Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	ı.	40979	Aaf55765 Recombina Aaf55766 PCR prime Aad14459 Recombina Acd28426 Wild type Acd38427 Engineere	Acd28605 Wild type Acd28606 Engineere Ad38193 Complemen Ad38192 DNA of a Ad60588 attBwt ol Aas06174 Phage-lam Aaf61422 AttB DNA Abz58727 Att site Acc59571 Nucleic a
SUMMARIES		AAX.78994 AAC55600 AAS06276 AAC87897 AAC87896	AAF55766 AAD14459 ACD28426 ACD28427 ACD28605	ACD28005 ADA38193 ADA38192 ADA060588 AAS06174 AAF61422 ABZ58727 ACCS9571
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## ALIGNMENTS

Site-specific recombination; bacterial attachment site; plasmid; vaccine; gene therapy; ss. A new expression cassette consists of a gene of interest controlled by a promoter and terminator functional in mammalian cells and is flanked by sequences in direct orientation which allow site-specific recombination. Lambda attp and attB sites specific recombination are the bacteriophage phage lambda. The expression cassettes can be used for producing plasmids which are useful in vaccination or for genetic/ cellular therapy, e.g. of amyotrophic lateral sclerosis; diseases of Plasmids capable of site-specific recombination - useful for vaccination and in gene therapy. coagulation/dyslipoproteinaemia or viral infections (AIDS or hepatitis) Wils P; Sequence 21 BP; 4 A; 4 C; 2 G; 11 T; 0 U; 0 Other; Scherman D, Darquet A, Claim 17; Page 43; 81pp; French. Bacteriophage lambda attB site. (RHON ) RHONE POULENC RORER SA. AAT37370 standard; DNA; 21 BP. 95FR-00002117. 96WO-FR000274. (first entry) Cameron B, Crouzet J, Bacteriophage lambda. WPI; 1996-402363/40. WO9626270-A1. 21-FEB-1996; 23-FEB-1995; 14-MAY-1997 29-AUG-1996. AAT37370; RESULT 1 AAT37370 

Query Match

Matches

AAF61417;

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The invention describes producing a collection of responder cells for high throughput screening assays, by identifying and cloning regulatory regions into expression constructs to control nucleic acids, and introducing the constructs into addressable cells. The method is useful introducing the constructs into addressable cells. The method is useful introducing cells used in high throughput screening assays for profiling substances and conditions and for studying the function of the regulatory tender the effects of any perturbation, such as external or internal condition, on the cells from which the regulatory regions in the reporter gene constructs are derived can be inferred. This sequence represents a constructs of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 producing a collection of responder cells for high throughput screening assays, comprises identifying and cloning regulatory regions into expression constructs to control nucleic acids, and introducing into
                                                           Responder cell; expression construct; screening assay; gene regulation;
blosensor; reporter gene construct; recombinase recognition site; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Length 21;
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                              Recombinase recognition site attB.
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12-MAR-2001; 2001US-0275148P.
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (I) a mucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites.
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                                                                                                                                                                                                                                                                                                                                                                Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attB; ds.
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                         Score 21; DB 2; Length 21;
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                                                                                                                                                                                                                                                                                                                                               coli attB DNA fragment.
                                                                   Conservative
                                                                                                                                                                                                                                     AAF61417 standard; DNA;
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С
                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
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RESULT 2

AAF61417

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AAF61417

AAF614

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WO200297059-A2.

ABS76597;

RESULT 3

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ABS76597

Matches

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Fleming E;

Leung J,

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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the Chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (Aces) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a ratificial chromosome, preferably an ACes. (II) is useful for producing continual (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection, micropiccille bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for an incleic acid that encodes a therapeutic product which is useful for an enterproper action of the production of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                    Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
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                                                                                                                                                                                                                                                            Perez C, Lindenbaum M, Greene A, Shellard J;
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                                                                                                                                                                                                      (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 6; 272pp; English.
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                                                                        30-MAY-2002; 2002WO-US017452.
                                                                                                                           30-MAY-2001; 2001US-0294758P.
21-MAR-2002; 2002US-0366891P.
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                                                                                                                                                                                                                                                      Perkins E,
Stewart S,
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The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination contains of the segments flanked by at least 2 recombination or contains of the segments of the set 2 recombination sites which do not recombine with each other; (2) one or more vector of recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombination efficiency with mutated attB2 site oligonucleotide attB0.
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                                                                                                                                                                       Disclosure; Page 176; 185pp; English.
                                                                              Temple GF,
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                                                                                                                                         New nucleic acid cloning methods.
                                             (LIFE-) LIFE TECHNOLOGIES INC.
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ID AAC55600 standard; DNA; 25 BP.
              98US-00177387.
 97US-0065930P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Conservative
                                                                             Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage lambda
                                                                                                          WPI; 1999-303011/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-543948/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200052027-A1.
24-OCT-1997;
              23-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC55600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Syntheti
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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attB2 concoling an attB1, attB2, attP1, attB2, attL1, attB2, attR1, and attB2 concoling an attB2 consprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination sites one provided att recombination sites, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites or myzising at least one mutated att recombination site and a second nucleic acid molecule comprising a second recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (1), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion tags from changing copy number, changing replicons, cloning into phages and changing copy number, changing replicons, cloning into phages and choose the process of the present sequence is used in the communities.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
Isolated nucleic acid molecules encoding an attB1, attB2, attB1, attL1, attL2, attL1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer attB0 used to produce a population of hybrid DNA molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 21; DB 3; Length 25; 100.0%; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Temple GF, Hartley JL, Byrd DRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                         Example 23; Page 157; 459pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lambda integrase; therapeutic; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CIGCITITITIALACTIG
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09-MAR-2000; 2000US-0188020P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-2000; 2000WO-US033546.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS06276 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRASCH M A.
TEMPLE G F.
HARTLEY J L.
BYRD D R N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriophage lambda
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200142509-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS06276;
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(TEMP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theo D,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PCR
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                                                                                                                                                             nucleic acid sequences, and PCR primers of the invention. The att sequences are recognised by the recombination protein lambda integrase (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising mixing at least a first population of hybrid acids comprising one or more recombination sites with at least one target nucleic acid comprising one or more recombination sites with at least one target nucleic acids the nucleic acids to recombine with all or some of the rarget nucleic acids. The method is useful for producing a population of hybrid nucleic acids which may be the same or different. The nucleic acids may be used to express therapeutic proteins or peptides and they may also be used to express therapeutic proteins or peptides and they may also be used to create novel fusion proteins by expressing different sequences linked to each other. The method allows simultaneous cloning of two or more different nucleic acids
                           Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins, e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered
                                                                                                                                                       AAS06174-AAS06322 represent Bacteriophage lambda att recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Core region, recombination site; cloning; chimeric DNA; PCR primer; characteristic; mutation; att site; lox site; phoA gene; ss.
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 4; Length 25; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Escherichia coli attB oligonucleotide SEQ ID NO:32.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                        Example 11; Page 227; 357pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 CTGCTTTTTATACTAACTTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Col 24; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGCTTTTTATACTAACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-00486139.
96US-00663002.
98US-00005476.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (LIFE-) LIFE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-00233493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC87897 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hartley JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-049004/06.
WPI; 2001-356174/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
07-JUN-1996;
12-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC87897;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC87897/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
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Comprising a first nucleic acid sequence having a defined sequence (IAAC87866 to AAC87881, sequences complementary to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881, are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site; (2) an isolated nucleic acid molecule (III) comprising a first at the recombination site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that enhances recombination specificity; (3) vectors (IV) comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in engineering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining consineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive. The present sequence represents an E. coli atts oligonuclectide, which is used in an example from the present invention
present invention describes an isolated nucleic acid molecule (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
   8X3355555555555555555555888
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100.0%; Score 21; DB 4; Length 25; 100.0%; Pred. No. 23; 0; Indels iive 0; Mismatches 0; Indels 1 CIGCTITITIATACTAACTIG 21 1 Similarity 100.0%; 21; Conservative C Query Match Local Best Loca Matches

0;

Gaps

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N 22 crecriririanacraacrie δ g

AAC87896 standard; DNA; 25 (first entry) 02-MAR-2001 AAC87896; RESULT 9 AAC87896 

Escherichia coli attB oligonucleotide SEQ ID NO:31.

Core region; recombination site; cloning; chimeric DNA; PCR primer; characteristic; mutation; att site; lox site; phoA gene; ss.

Escherichia coli.

JS6143557-A.

07-NOV-2000.

99US-00233493. 20-JAN-1999;

Hartley JL, Brasch MA; WPI; 2001-136877/14.

> 95US-00486139. 98US-00005476. 96US-00663002 07-JUN-1995; 12-JAN-1998; 07-JUN-1996

LIFE-) LIFE TECHNOLOGIES INC.

WPI; 2001-049004/06.

Brasch MA, Hartley JL;

Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered

Example 3; Col 24; 73pp; English.

mutation.

The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AAC87866 to AAC87881, sequences complementary to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first

ó recombination site or avoids hairpin formation, the recombination site being an att or lox site; (2) an isolated mucleic acid molecule (III) comprising a first att recombination site comprising a mutation that enhances recombination specificity; (3) vectors (IV) comprising the above mentioned nucleic acids, and (4) cells comprising the above mentioned nucleic acids are used in engineering a corregion of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive. The present sequence represents an E. coli attB oligonuclectide, which is mutated recombination site that removes one or more stop codons from the Gaps .; 100.0%; Score 21; DB 4; Length 25; 100.0%; Pred. No. 23; 0; Indels Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other; used in an example from the present invention Mismatches Recombination site; cloning; att; ss. 1 CTGCTTTTTTATACTAACTTG 21 24 .; 0 4 CTGCTTTTTTATACTAACTTG (LIFE-) LIFE TECHNOLOGIES INC. AAF55765 standard; DNA; 25 BP 95US-00486139. 96US-00663002. 98US-00005476. 12-APR-2001 (first entry) Recombination site attBwt. 21; Conservative Best Local Similarity 12-JAN-1998; 07-JUN-1995; Unidentified US6171861-B1 09-JAN-2001. AAF55765; Matches RESULT 10 **AAF5576**5 à g 

The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture, and selecting for a host comprising the chimeric nucleic acid molecule, and selecting against a host comprising the vectors comprising the second vector; to clone the nucleic acid. The present sequence is a recombinantion site, which may be used in the method of the present In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host. Example 3; Col 23; 73pp; English invention φ

Matches

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The invention relates to a method for apposing an expression signal and a gene or partial gene, using recombinatorial cloning. The method incubates nucleic acids comprising the expression signal and the gene/ partial gene in the presence of a recombination protein under conditions sufficient to cause recombination and therefore appose the expression signal and the gene or partial gene using recombinatorial cloning. The methods are useful for apposing an expression signal and a gene or partial gene using recombinatorial cloning. The methods are also useful for changing vectors, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages, and cloning e.g., PCR products (with an attB site at one end and a loxe site at the other end), genomic DNAs. The methods are highly specific, rapid, and less labour intensive than prior art methods. The present sequence is a recombination site useful for recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Methods for apposing nucleic acids comprising an expression signal and a gene/partial gene, using recombinatorial cloning by incubating the nucleic acids in the presence of a recombination protein under conditions for recombination.
                                                                                                                        site; copy number; replicon; recombinatorial cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 4; Length 25; Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wild type attL and attR site recombination sequence attB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vector donor DNA; ds; flanking recombination site; attB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                               Recombination site attBwt wild type DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIGCTTTTTATACTAACTIG 24
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                                      (first entry)
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Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            (INVI-) INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brasch MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-488248/53.
                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                              US6270969-B1
                                                                                                                                                                                                                                                                                                           20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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                                      01-NOV-2001
                                                                                                                                                                                                                                                                    07-AUG-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hartley JL,
                                                                                                                                              attBwt; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
  AAD14459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACD28426;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting against a host comprising the vectors comprising the second vector, to clone the nucleic acid. The present sequence is a PCR primer used in the method of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                    Gaps
                                                                                 0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 21; DB 4; Length 25; 100.0%; Pred. No. 23; ive 0; Mismatches 0; Indels
                                  100.0%; Score 21; DB 4; Length 25; 100.0%; Pred. No. 23; o; Indels ive 0; Mismatches 0; Indels
Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombination site; cloning; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Col 43-44; 73pp; English.
                                                                                                                      1 CTGCTTTTTTATACTTG 21
                                                                                                                                                CTGCTTTTTATACTAACTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGCTTTTTTATACTAGCTTG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CIGCITITITATACIAACIIG 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAD14459 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                    ВЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 100.0%;
Conservative 0
                                                          l Similarity 100.0%;
21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-00005476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-00486139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-00663002.
                                                                                                                                                                                                                                                                AAF55766 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brasch MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-136877/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                         PCR primer #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUN-1995;
07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US6171861-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2-JAN-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hartley JL,
                                                                                                                                                                                                                                                                                                                                                12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-JAN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                         AAF55766;
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                                      Query Match
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Gaps

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0; Indels

Matches

RESULT 12 AAD14459 ID AAD1 XX

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07-JUN-1995;
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20-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-APR-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACD28605;
                                                                                                                                                        marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 15
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                                                                                                                                                                                                                                                                                                                                         The invention relates to a vector donor DNA molecule comprising a first DNA segment and a second DNA segment containing at least one selectable marker. The first and second segments are separated either by, in a clircular vector donor, a first and a second recombination site, or in a linear vector donor, at least a first recombination site, where each pair of flanking recombination sites are engineered and do not recombine with each other. The nucleic acid molecule, vectors and methods are useful for moving or exchanging segments of DNA molecules using engineered moving or exchanging segments of DNA molecules using engineered molecules that have the desired characteristic(s) and/or DNA segment(s).
                                                                                                                                                                                                                                             New Vector Donor DNA molecule for recombinational cloning using engineered recombination sites, comprises first and second DNA segments that do not recombine with each other and that contain a Selectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence represents the wild type attL and attR site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vector donor DNA; ds; flanking recombination site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Engineered recombination site associated DNA #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21; DB 8
Pred. No. 23;
; Mismatches
                                                                                                                                                                                                                                                                                                                     Example 3; Page 13; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGCTTTTTTATACTAG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      th 100.0%; So 150.0%; Bo 21; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 crecirririraracrascric
                                                                             95US-00486139.
96US-00663002.
99US-00233493.
99US-00432085.
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96US-00663002.
99US-00233493.
99US-00432085.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               427/c
ACD28427 standard; DNA; 25 BP
                                                     2002US-00058291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2002US-00058291.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombination sequence attB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                          Hartley JL, Brasch MA;
                                                                                                                                                 (HART/) HARTLEY J L.
                                                                                                                                                                                                                      WPI; 2003-540791/51
                                                                                                                                                               BRASCH M A.
US2003064515-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US2003064515-A1.
                                                   30-JAN-2002;
                                                                                                        20-JAN-1999;
02-NOV-1999;
                                                                             07-JUN-1995;
                                                                                             07-JUN-1996;
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20-JAN-1999;
02-NOV-1999;
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                         03-APR-2003
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                                                                                                                                                               BRAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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The invention relates to a vector donor DNA molecule comprising a first DNA segment and a second DNA segment containing at least one selectable marker. The first and second segments are separated either by, in a circular vector donor, a first and a second recombination site, or in a linear vector donor, at least a first recombination site, where each pair of flanking recombination sites are engineered and do not recombine with each other. The nucleic acid molecule, vectors and methods are useful for moving or exchanging segments of DNA molecules using engineered
                                                                                                                                                                                                                                                                               segments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           recombination sites and recombination proteins to provide chimeric DNA molecules that have the desired characteristic(s) and/or DNA segment(s). The present sequence represents the engineered recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                          New Vector Donor DNA molecule for recombinational cloning using engineered recombination sites, comprises first and second DNA segmethat do not recombine with each other and that contain a Selectable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Making Cointegrate DNA molecule, by combining recombination sites flanking the desired DNA segment in insert donor DNA, with the recombination sites of vector donor DNA, using site specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wild type attL and attR site recombination sequence attBwt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 21; DB 8; Length 25;
Pred. No. 23;
; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cointegrate DNA; flanking recombination site; ds; attBwt.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 25 BP; 11 A; 3 C; 5 G; 6 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure, Page 24; 71pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
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96US-00663002.
99US-00233493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
                                                                                                  Hartley JL, Brasch MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (INVI-) INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hartley JL, Brasch MA;
HART/) HARTLEY J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-540884/51.
                                                                                                                                                              WPI; 2003-540791/51
                               (BRAS/) BRASCH M A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  associated DNA #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US2003068799-A1.
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Sequence 25 BP; 6 A; 5 C; 3 G; 11 T; 0 U; 0 Other;

Query Match

Best Local Similarity 100.0%; Pred. No. 23;

Matches 21; Conservative 0; Mismatches 0; Indels

| CTGCTTTTTTTATACTAACTTG 21
| CTGCTTTTTTTATACTAACTTG 24
| CTGCTTTTTTTTATACTAACTTG 24

95 da

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0; Gaps

Search completed: September 9, 2004, 18:05:38 Job time : 25.9144 Secs

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Sequence 13, Appl
Sequence 95, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 31, Appl
Sequence 32, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 60, Appl
Sequence 60, Appl
                                                                                                      9, 2004, 19:34:38; Search time 26.5292 Seconds (without alignments) 3962.858 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6, Al
Sequence 34, 1
Sequence 45, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/USOO_NEW PUB.seq:*
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18: /cgn2_6/ptodata/2/pubpna/USOO_NEW PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USOO_NEW PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-252-384-6
US-10-161-403-45
US-10-97-034A-45
US-09-73-914-95
US-09-97-2914-95
US-09-907-900-60
US-09-907-900-60
US-09-907-719-60
US-09-432-085-31
US-09-432-085-31
US-09-432-48-60
US-10-680-316-60
US-10-680-316-60
                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                         3304383 seqs, 2515761380 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                      using sw model
                                                                                                                                                                                                                 1 ctgcttttttatactaacttg 21
                                                                                                                                                                                                                                                   IDENTITY_NUC Gapop 10.0
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21
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Sequence 31, Appl
Sequence 32, Appl
Sequence 22, Appl
Sequence 60, Appl
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Sequence 1, Appli
Sequence 19, Appl
Sequence 23, Appl
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Sequence 54, Appl
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Sequence 8, Appli
                                                                                                                                                                                                                                       Sequence 11,
                                                                                                                                                                                                                      Sequence 74,
Sequence 13,
       Sequence
                                                                                                                                                                                                                 Sequence
                                                                          US-09-732-914-1

US-10-301-849A-19

US-10-301-849A-19

US-10-627-711-23

US-10-627-711-23

US-10-627-711-23

US-10-61-403-8

US-10-161-403-9

US-10-161-403-9

US-10-403-232-55

US-10-403-232-55

US-10-403-232-105

US-10-252-384-1

US-10-252-384-1
                    US-10-162-879-31
VS-10-162-879-32
US-10-300-892-60
US-10-627-711-22
US-10-815-730-60
US-10-820-133-60
US-10-627-711-4
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US-09-981-803-13
US-10-627-711-11
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## ALIGNMENTS

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Sequence 3, Application US/09981803
FUDICATION NO. USZ0030032092A1
GENERAL INFORMATION
APPLICANT: Deal SCHERMAN
APPLICANT: Daniel SCHERMAN
APPLICANT: Din NOLECULES, PREPARATION AND USE IN GENE THERAPY
TITLE OF INVENTION DNA MOLECULES, PREPARATION AND USE IN GENE THERAPY
FILE REPERENCE: MINICIRCLE
CURRENT APPLICATION NUMBER: US/09/981, 803
CURRENT FILING DATE: 201-10-19
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of the artificial sequence: OTHER INFORMATION: oligonucleotide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Conservative
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US-09-981-803-3
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                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO 3
LENGTH: 21
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Best Local S:
Matches 21
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RESULT 2 US-10-252-384-6 ; Sequence 6, Application US/10252384

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21

CTGCTTTTTATACTAACTTG

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us-10-014-45

i Sequence 45, Application US/10097034A

i Sequence 45, Application US/10097034A

publication No. US20040076954A1

general information

i APPLICANT: Su, Andrew

APPLICANT: Su, Andrew

APPLICANT: Caldwell, Jonem

i TITLE OF INVENTION: Collections of Cellular Reporters

I TITLE OF INVENTION: UNMBER: US/10/097,034A

CURRENT RELING DATE: 2001-03-12

PRIOR FILING DATE: 2001-03-12

NUMBER OF SEQ ID NOS: 56

SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-310-695-13
Sequence 13, Application US/10310695
Publication No. US20040110293A1
GENERAL INFORMATION:
APPLICANT: DROGE, PETER
APPLICANT: ENENKEL, BARBARA
TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN BUKARYOTIC CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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Pred. No. 18:
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Pred. No. 18;
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                   FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
PRIOR PEDLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR PELING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FASTSEQ for Windows Version 4.0
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100.0%; Pr
vative 0;
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Best Local Similarity 100.0
Matches 21, Conservative
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; OTHER INFORMATION: attB
US-10-161-403-34
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US-10-097-034A-45
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                           WILS, Pierre
DARQUET, Anne-Marie
DARQUET, Anne-Malie
TITLE OF INVENTION: DNA MOLECULES, PREPARATION THEREOF AND
USE THEREOF IN GENE THERAPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/252,384
FILING DATE: 24-Sep-2002
CLASSIFICATION: CURROWD>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: SAVIEZRY ESQ., MARTIN F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95013-US
TELECOMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: «Unknown»
APPLICATION NUMBER: FR 95/02117
FILING DATE: 23-EB-1995
APPLICATION NUMBER: WO FR96/00274
FILING DATE: 21-FBB-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 34, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION:
APPLICANT: Perkins, Edward
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Blena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (610) 454-3816
(610) 454-3808
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                                                                SCHERMAN, Daniel
CAMERON, Beatrice
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STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (610) 454-
INFORMATION FOR SEQ ID NO: 6:
Publication No. US2003010444A1
                   GENERAL INFORMATION:
APPLICANT: CROUZET, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Greene, Amy
Leung, Josephine
Fleming, Elena
Stewart, Sandra
Shellard, Joan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-161-403-34
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gard.
APPLICANT: Temple, Gard.
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/907,900
CURRENT FILING DATE: 1998-10-7-19
PRIOR PILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
IENGTH: 25
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Publication No. US2020192819A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Garry F.
APPLICANT: Soc. Donna K.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE REPERENCE: 0942.285004
CURRENT APPLICATION NUMBER: US/09/907,719
CURRENT FILING DATE: 2001-07-19
                                                                                                                                                                                                                                                                                                                                                                    Gaps
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OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
                                                                                                                                                                                                        OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 21; DB 9; Length 25; Best Local Similarity 100.0%; Pred. No. 19; Matches 21; Conservative 0; Mismatches 0; Indels
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PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 60, Application US/09907900 Patent No. US20020172997A1
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PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 60
LENGTH: 25
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Best Local Similarity 100.0
Matches 21, Conservative
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ORGANISM: Unknown
                                                                                                                                                            ORGANISM: Unknown
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US-09-907-719-60
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                                                                                                                                       TYPE: DNA
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Sequence 95, Application US/09732914

Patent No. US20020007051A1

Sequence 95, Application US/09732914

Patent No. US20020007051A1

APPLICANT: Cheo, David

APPLICANT: Ensek, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Bartley, James L.

APPLICANT: Byrd, Devon R.N.

TITLE OF INVENTION: Recombinational Cloning

FILE REFERENCE: 0942.5010002

FILE REFERENCE: 0942.5010002

FILE REFERENCE: US 60/169,983

PRIOR APPLICATION NUMBER: US 60/169,983

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 140

SOFTWARE: PatentIn version 3.0

SEQ ID NO 95

LEGGTH: 25

LEGGTH: 25
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APPLICANT: Bratley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Ferple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942-22850006
CURRENT APPLICATION NUMBER: US/09/855,797A
PRIOR APPLICATION NUMBER: 09/296,281
PRIOR APPLICATION NUMBER: 09/296,281
PRIOR FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: US 60/065,930
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  FILE REFERENCE: DEBE:019US
CURRENT APPLICATION NUMBER: US/10/310,695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 13
LENGTH: 21
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                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCTTTTTTATACTAACTTG 21
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Best Local Similarity 100.0%;
Matches 21; Conservative 0;
                                                                                                                                                                                       ; TYPE: DNA; ORGANISM: Escherichia coli
US-10-310-695-13
                                                                                                                                                                                                                                                                                                                    Best Local Similarity 100.
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; ORGANISM: attB0
US-09-732-914-95
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Gaps
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                                                                                                                                                                                                                                                                                                          | Sequence 32 Application US/09432085 | Sequence 32 Application US/09432085 | Publication No. US20030100110A1 |
| Fublication No. US20030100110A1 |
| GENERAL INFORMATION: Hartley, James L. APPLICANT: Hartley, James L. APPLICANT: Brasch, Michael A. TITLE OF INVENTION: Recombinational Cloning Using Engineered | TITLE OF INVENTION: Recombination Sites | NUMBER OF SEQUENCES: 35 | CORRESPONDENCE ADDRESSE: STERNE, KESSIER, COLDSTEIN & FOX, P.L.L.C
                                      Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 25;
                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
TITING DATE: (Herewith)
                                   Score 21; DB 10;
Pred. No. 19;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 21; DB 10; 100.0%; Pred. No. 19;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECHOMENICATION:
TELECHOMENICATION:
TELECHOME: 202-371-260
TELEFAX: 202-371-260
TELEFAX: 202-371-2540
TELEFRAX: 202-371-2540
TELEFAX: 202-371-2540
TELEFAX: 202-371-2540
TELEFAX: 202-371-2540
TELEFAX: 202-371-260
TELEFAX: 202-371-260
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
           100.0%; Scu
100.0%; Pre
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                                                                                                                                                                                                        4 CIGCILITITATACTACTIG 24
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                                   Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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Best Local Similarity 100.0
Matches 21; Conservative
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MOLECULE TYPE: CDNA
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US-09-432-085-32
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                                                                                                                                                                                                ) OTHER INFORMATION: Description of Unknown Organism: recombination; OTHER INFORMATION: products
US-09-907-719-60
                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 31, Application US/09432085
Publication No. US20030100110A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                                                                                                                                                                                                                                                                                                      Length 25
                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 20005-3934

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
OPERATING SYSTEM:
APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FLING DATE: (Herewith)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FLING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 09/663,002
FLING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR 
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Pred. No. 19;
                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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APPLICATION NUMBER: 08/486,13
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
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INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 60
LENGTH: 25
                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                TYPE: DNA
ORGANISM: Unknown
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; MOLECULE TYPE:
US-09-432-085-31
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US-09-432-085-31
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TITLE OF INVENTION: Recombinational Cloning Using Engineered Recombination Sites
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Publication No. US20030064515A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURREATING SYSTEM: PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,291
FILING DATE: 30-Jan-2002
CLASSIFICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/05,476
FILING DATE: 20-JAN-1998
APPLICATION NUMBER: 08/653,002
APPLICATION NUMBER: 08/653,002
APPLICATION NUMBER: 08/653,002
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                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS: ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombination Sites
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
                        4 CIGCITITITATACTAACTIG 24
                                                                                                                                                                                      Sequence 31, Application US/10058291
Publication No. US20030064515A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                 APPLICANT: Hartley, James L. Brasch, Michael A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: 202-371-2600
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 21; Conservative
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                                                                                                                       RESULT 14
US-10-058-291-31
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US-09-985-448-60

US-09-985-448-60

Sequence 60, Application US/09985448

Publication No. US20030157716A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.285004

CURRENT APPLICATION NUMBER: US/09/985,448

CURRENT APPLICATION NUMBER: US/09/177,387

PRIOR FILING DATE: 1998-10-23

PRIOR APPLICATION NUMBER: US 60/065,930

PRIOR APPLICATION NUMBER: US 60/065,930

NUMBER OF SEQ ID NOS: 60

SEQ ID NO 60

LENGTH: 25

LENGTH: 25

LENGTH: 25
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Fublication No. US20040063207A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Pox, Donna K.

TITLE OF INVENTION: Recombination Sites

FILE REFRENCE: 0942.2850004

CURRENT APPLICATION NUMBER: US/09/177,387A

FRICR APPLICATION NUMBER: US/09/177,387A

FRICR APPLICATION NUMBER: US/09/177,387A

FRICR FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 60

LEMBET 25

LEMBET 35

LEMBET 35
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US-10-680-316-60
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Best Local Similarity 100.
Matches 21; Conservative
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ORGANISM: Unknown
FEATURE:
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ORGANISM: Unknown
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Indels

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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
COUNTY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: PEADABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0.058,291
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-03
APPLICATION NUMBER: 09/233,493
FILING DATE: 1999-11-03
APPLICATION NUMBER: 09/233,493
FILING DATE: 1999-11-03
APPLICATION NUMBER: 09/486,139
FILING DATE: 10-JAN-1996
APPLICATION NUMBER: 09/486,139
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 09/486,139
FILING DATE: 07-JUN-1995
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

100.0%; Score 21; DB 13; Length 25;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 21; Conservative 0; Mismatches 0; Indels
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MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-10-058-291-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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Search completed: September 10, 2004, 00:14:06 Job time : 27.5292 secs

à Db

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Gaps

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September 9, 2004, 15:48:15; Search time 144.957 Seconds (without alignments) 6279:120 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3470272 segs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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1 ctgctttttatactaacttg 21
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1: gb_ba:*

2: gb_htg:*

4: gb_on:*

5: gb_ov:*

5: gb_ov:*

7: gb_pt:*

8: gb_pt:*

8: gb_pt:*

9: gb_
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em_htgo_other:*
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                       Run on:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AR265736 Sequence	AR124551 Sequence	AR124552 Sequence	ARI63202 Sequence AR163203 Sequence	BD263313 Compositi	AX4916/0 Sequence AX498641 Sequence	BD131386 Recombina	AR142201 Sequence AR142202 Sequence	A46167 Sequence 5	A46168 Sequence 6 AR361092 Sequence	AR361093 Sequence	AX787502 Sequence	AK265/31 Sequence AR265732 Sequence	AR265752 Sequence	AR142204 Sequence AR142203 Sequence	AR265753 Sequence	BD131357 Recombina	U39938 Escherichia	AR131048 Sequence	BD235468 Control o AR261940 Sequence	AR350177 Sequence	AR131049 Sequence BD235469 Control o	AR261941 Sequence	AR350178 Sequence	A38251 Sequence 6	A93674 Sequence 1	AR101809 Sequence	AR101810 Sequence	AE000180 Escherich	AX787504 Sequence	AX787505 Sequence BD263306 Compositi		linear PAT 10-APR-2003			Wils,P. and Darquet,AM. : gene transfer
SUMMARIES	AR265736	AR124551	AR124552	AR163202 AR163203	BD263313	AX491670 AX498641	BD131386	AK142201 AR142202	A46167	A46168 AP361092	AR361093	AX787502	AR265731 AR265732	AR265752	AR142204	AR265753	BD131357	ECU3 9938	AR131048	BD235468 AR261940	AR350177	AR131049 RD235469	AR261941	AR350178	A38251	A93674	A33879 AR101809	AR101810	œμ	10	AX787505 BD263306	ALIGNMENTS	-	US 6492164.		, Cameron,B., W. cassettes for 10-DEC-2002; fiers
Length DB	1																											5872		27	27 6 30 6			6 from patent 1 GI:2969457	,	ried. s 1 to 21) J., Scherman, D., DNA expression US 6492164-A 6 1 Location/Qualif
% Query ore Match	100.0		100	100		100	100	100	100	100.	100	100.	100.	100.	100	100.	100.	100.	100.	100.	100.	100.	100.	100.	100.	100.	100	100	100.	.4 92.	9.4 92.4 9.4 92.4		38789688		Unknown. Unknown.	Unclassified  (bases 1 Crouzet, J., Circular DNA Patent: US 6
Result No. Scor	; ; ; ;	7 m	ນ <b>4</b>		0	သောက	10	c 12		ο 41.	c 16	17			G 21		24	c 25		28 29	30	31	3 K			C 37			41	1	444 145		RESULT 1 AR265736	DEFINITION ACCESSION VERSION	KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOURNAL FEATURES

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PAT 16-MAY-2001
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: US 6171861-A 32 09-JAN-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Unclassified.
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
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Lases 1 to 25)

Hartley, J.L. and Brasch, M.A.

Recombinational cloning using enginee

Patent: US 6270969-A 31 07-AUG-2001;

Location/Qualifiers
                                                     25 bp 1
AR124552
AR124552.1 GI:14109913
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 31 from patent US 6270969.
AR165202 AR163202.1 GI:16233722
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 32 from patent US 6270969.
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AR163203.1 GI:16233725
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Unclassified.
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Best Local Similarity
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                             RESULT 4
AR124552/c
LOCUS
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                                                                      DEFINITION
ACCESSION
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AR163203/c
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ACCESSION
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TITLE
JOURNAL
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AR163202
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                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: US 6171861-A 31 09-JAN-2001;
Location/Qualifiers
                                                                                                    ..
                                                                                                                                                                                                                                                                                                                                                                                            Sequence-specific dna recombination in eukaryotic cells Patent: WO 0116345-A 1 08-MAR-2001; Droege, Peter (DE) Location/Qualifiers
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                                                                      Length 21;
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100.0%; Score 21; DB 6; Length 21;
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 21; Conservative 0; Mismatches 0; Indels
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1 Similarity 100.0%; Pred. No. 5.5e+02;
21; Conservative 0; Mismatches 0; Indels
                                                                   Query Match 100.0%; Score 21; DB 6; I
Best Local Similarity 100.0%; Pred. No. 5.8e+02;
Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                      DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Escherichia coli"
/mol_type="unassigned DNA"
/db xref="taxon:562"
1. .21
/organism="unknown"
/mol_type="unassigned DNA"
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 31 from patent US 6171861.
AR124551
                                                                                                                                                                                                                               Sequence 1 from Patent WO0116345.
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Escherichia coli
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AR124551
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BD131386 25 bp DNA linear PAT 18-SEP-2002
Recombinational cloning using nucleic acids having recombination
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Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.

Hartley, J.L., absorbing using nucleic acids having recombination Patent: JP 2002500861-A 60 15-JAN-2002;

LIFE TECHNOLOGIES INC
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PD 15-JAN-2002
PF 26-OCT-1999 JP 200518069
PR 24-OCT-1997 US 66/065530,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
                                                                                                                                                                                                                                                    Gaps
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Recombinational cloning using engineered recombination sites
Patent: BP 1229113-A 31 07-AUG-2002;
INVITROGEN CORPORATION (US)
Location/Qualifiers
                 engineered recombination sites
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engine
Patent: EP 1227147-A 31 31-JUL-2002;
INVITROGEN CORPORATION (US)
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/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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'... 0; Mismatches
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/organism="unidentified"
/mol_type="unassigned DNA"
/db_xref="taxon:32644"
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Sequence 31 from Patent EP1229113.
AX498641
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JP 2002500861-A/60.
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AX498641
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DN Artificial Sequence
PN JP 2002537790-A/91
PD 12-NOV-2002
PP 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,CO7K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/ PC
00,C12N5/00
CC attB0
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FF Key
Location/Qualifiers
FT source
/ Organism='Artificial Sequence'.
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1 (Dases 1 to 25)
Hartley,J.L. Brasch,M.A., Temple,G.F. and Cheo,D.
Compositions and methods for use in recombinational cloning of
nucleic acids
Patent: JP 2002537790-A 91 12-NOV-2002;
INVITROGEN CORP
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                                                                                                                                     Score 21; DB 6; Length 25; Pred. No. 5.5e+02;
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        Corganism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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100.0%; Pred. No. ...
0; Mismatches
 Patent: US 6270969-A 32 07-AUG-2001;
Location/Qualifiers
                                                                               /mol_type="unassigned DNA"
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AX491670
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                                         1. .25
/organism="unknown"
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JP 2002537790-A/91.
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RESULT 8 AX491670 ORGANISM

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DEFINITION RESULT 7 BD263313/c

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PAT 07-MAR-1997
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Sodoyer,R., Aujame,L. and Geoffroy,F.
METHOD FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF ANTIBODY GENE
PERPRESSION VECTORS
PATENT: MO 9521914-A 5 17-AUG-1995,
PASTEUR MERIEUX SERUMS VACC (FR)
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Sodoyer,R., Aujame,L. and Geoffroy,P.
Sodoyer,R., Aujame,L. and Geoffroy,P.
METHOD FOR PREPARING A MULTICOMBINATORIAL LIBRARY OF ANTIBODY GENE
PARTESSION VECTORS
PARTEUN O 9521914-A 6 17-AUG-1995,
PASTEUR MERLEUX SERUMS VACC (FR)
Other publication FR 2715940 950811.
Location/Qualifiers
                                                     Gaps
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100.0%; Score 21; DB 6; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels
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                               Best Local Similarity 100.0%; Pred. No. 5.4e+02; Matches 21; Conservative 0; Mismatches 0;
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Pred. No. 5.4e+02;
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Other publication FR 2715940 950811.
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/db_xref="taxon:32644"
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/db_xref="taxon:32644"
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A46167
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/organism="unidentified"
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Sequence 6 from Patent WO9521914.
A46168
A46168.1 GI:2300416
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Matches 21; Conservative
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C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1...25
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Unclassified.
1 (bases 1 to 26)
Sodoyer, R., Aujame, L., Geoffroy, F. and Bouchardon, A.
Preparation of a multicombinatorial library of antibody gene
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Sodoyer,R., Aujame,L., Geoffroy,F. and Bouchardon,A.
Preparation of a multicombinatorial library of antibody gene
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Pred. No. 5.5e+02;
Mismatches 0; Indels
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                                                                                              /organism='Unknown'
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/mol_type="unassigned DNA"
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AR142202.
AR142202.1 GI:15102502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      expression vectors
Patent: US 6174708-A 7 16-JAN-2001;
Location/Qualifiers
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Patent: US 6174708-A 8 16-JAN-2001;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 7 from patent US 6174708.
ARI42201.
ARI42201.1 GI:15102501
                                                                                                                                  1. .25
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/db_xref="taxon:32644"
                                                                                                                                                                                                                                                                                                                   1 CTGCTTTTTTATACTTG 21
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Unclassified.
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DEFINITION

ACCESSION VERSION KEYWORDS

RESULT 11

à a AR142201

SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL

FEATURES

ORIGIN

RESULT 12 AR142202/c LOCUS

DEFINITION ACCESSION VERSION KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE

JOURNAL FEATURES

ORIGIN

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21 CTGCTTTTTTATACTAG 1

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Unknown.

(ISM Unknown.

Unclassified.

NCE 1 (bases 1 to 27)

IORS Sodoyer,R., Aujame,L. and Geoffroy,F.

LE Process for preparing a multicombinatorial library of vectors for expressing antibody genes

URMAL Patent: US 6595697-A 5 29-UUL-2003;

Location/Qualifiers

Location/Qualifiers

1. 27

/organism="unknown"
/mol_type="genomic DNA"
                                  PAT 17-AUG-2003
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 21; Conservative 0; Mismatches 0; Indels
                                  linear
                                  DNA
                               AR361092 27 bp
Sequence 5 from patent US 6599697.
AR361092 AR361092.1 GI:33768795
RESULT 15
AR361092
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWOEDS
SOURCE
ORGANISM
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AUTHORS
TITLE
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1 CTGCTTTTTATACTAACTTG 21

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Search completed: September 9, 2004, 19:34:27 Job time: 146.957 secs

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APPLICANT:
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STATE:
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Sequence 31,
Sequence 32,
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'GgnZ_6/ptodata/2/ina/5A_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-101-629A-7
US-09-101-629A-8
US-08-693-234-5
US-08-693-234-5
US-08-894-511-1
US-09-655-728-1
US-09-655-728-1
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US-09-233-493-32
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US-09-101-629A-9
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect :
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## ALIGNMENTS

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Sequence 6, Application US/08894511

Sequence 6, Application US/08894511

Sequence 6, Application US/08894511

Patent No. 6143530

GENERAL INFORMATION:

APPLICANT: CROUZET, Joel

APPLICANT: CREENAN, Daniel

APPLICANT: PARENOW, Beatrice

ADDRESSEB: Rhone-Poulenc Rorer Inc.

APPLICANT: Collegeville

STATE: 19426

CONDURY: USA

ZIP: 19426

COMPUTER: IBM PC compatible

COMPUTER: IBM PC COMPUTER: ISM PC COMPUTER: IBM PC COMPUTER: ISM PC CO
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Sequence 31, Application US/09233493
Patent No. 6145357
Patent No. 6145377
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                          CITY: Washington
STATE: DC
COMPUTRY: USA
ZIP: 2005-3934
ZIP: 2005-3934
ZIP: 2005-3934
COMPUTER READABLE FORM:
RELIUM TYEE: IBW PC COMPATIBLE
COMPUTER: IBW PC COMPATIBLE
COMPUTER: PARCHININ RELEASE #1.0, Version #1.30
SOFTWARE: Petentin Release #1.0, Version #1.30
CURRENT ADPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 12-JAN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
CLASSIFICATION:
PRIOR APPLICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INF
                                                                                                                                                                                                                                                                                                                            ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CTGCTTTTTTATACTAG 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IDEN PC compatible
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/655,728
FILING DATE: 05-Sep-2000
CLASSIFTCATION: cUnknown>
PROPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/894,511
FILING DATE: cUnknown>
APPLICATION NUMBER: WO FR96/00274
FILING DATE: 21-FEB-1996
ATTORNEY/AGENT INFORMATION:
                                                                  Score 21; DB 3; Length 21; Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 21; DB 4; Length 21; Pred. No. 1.5;
                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Road, Mailstop 3C43
CITY: Collegeville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Oligonucleotide"
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Savitzky Esq., Martin F.
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST95013-US
                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SCHERMAN, Daniel
CAMERON, Beatrice
WILS, Pierre
DARQUET, Anne-Marie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 454-3816
                                                                                                                                                                                             1 CTGCTTTTTTATACTAACTTG 21
                                                                                                                                                                                                                                                         1 crecriririaractaactic 21
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Patent No. 6492164
GENERAL INFORMATION:
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1 Similarity 100.0%;
21; Conservative 0
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: CROUZET, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                           Query Match
Best Local Similarity
Matches 21; Conserv
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Best Local Similarity
Matches 21; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                RESULT 2
US-09-655-728-6
US-08-894-511-6
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Patent No. 6143557
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERME, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
Query Match
100.0%; Score 21; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels
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Gaps

0,

Indels

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Mismatches

0;

21; Conservative

1 CTGCTTTTTTATACTAACTTG 21 CTGCTTTTTATACTAACTTG 21

RESULT 3

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0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                        CIGCITITITATACIACTIG 24
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; Sequence 32, Application US/09005476
; Patent No. 6171861
                                                                                                                                                                                                                                                                                                                                       1 CIGCTITITIATACTAACTIG 21
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                 TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 31:
SEQUIENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22 CTGCTTTTTATACTACTTG
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-233-492-31
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Fatent No. 6171861
GENERAL INFORMATION.
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEB: STERNE, KESSLER, GOLDSTRIN & FOX, P.L.L.C.
STREET: 1100 New YORK Ave., N. W. Suite 600
CITY: Washington
STATE: DC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENY APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                    CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRICR APPLICATION:
PRICR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
CLASSIFICATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0%;
Matches 21; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGIH: 25 base pairs
                 ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: CDNA
US-09-233-493-32
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US-09-005-476-31
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
Query Match
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 21; DB 3; Length 25; 100.0%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: MS/09/005,476
FILING DATE: herewith
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FACULANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REPERENCE: 0942.2865007
CURRENT FILING DATE: 1999-04-22
BARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1999-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Unknown Organism: recombination; OTHER INFORMATION: products
US-09-296-280-60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/233,492 FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                         APPLICATION DATA:
PRIOR DATE: 20-JAN-1999
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 202-371-2640
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
              OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CIGCTITITIATACTAACTIG 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 60, Application US/09296280 Patent No. 6277608
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Best Local Similarity 100.0%;
Matches 21; Conservative 0
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Best Local Similarity 100.(
Matches 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: bot
; MOLECULE TYPE:
US-09-233-492-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-296-280-60
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LENGTH: 25
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Sequence 31, Application US/09233492
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEB: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
COUNTRY: Washington
STATE: COOLSTEE FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: FORM:
MEDIUM TYPE: Batenin Release #1.0, Version #1.30
CORPUTER: Patenin Release #1.0, Version #1.30
FILING DATE: 20-JAN-1999
FILING DATE: 20-JAN-1999
FILING DATE: 20-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAIL:
COUNTRY: USA
ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 8
US-09-233-492-32/c
'Sequence 32, Application US/09233492
'Patent No. 6270969
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CTGCTTTTTTATACTAG 21
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INPORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 both
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APPLICANT: 116 Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

Query Match

100.0%; Score 21; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 21; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPRIATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
                                                                                                                                                                                                           PILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 08/663,002
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1996
CLASSIFICATION TO DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SQL 12-2600
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                ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CTGCTTTTTTATACTACTTG 21
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ZIP: 20005-3934
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-498-074-32
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Fatent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ·;
                                                                                     APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEGUENCE: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 21; DB 4; Length 25; Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  Sequence 31, Application US/09498074 Patent No. 6534264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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STRANDEDNESS: both
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Best Local Similarity
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                                                                        GENERAL INFORMATION:
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; MOLECULE TYPE:
US-09-498-074-31
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US-09-498-074-31
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Gaps

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Search completed: September
Job time : 5.63035 secs
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                                                                                                                   SEQ ID NO 8
LENGTH: 26
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APPLICANT: Sodoyer, Regis
APPLICANT: Sodoyer, Regis
APPLICANT: Sodoyer, Dr. Sodoyer, Bedis
APPLICANT: Authoriane, Luc
APPLICANT: Geoffroy, Lrederique
APPLICANT: Bouchardon, Annabelle
TITLE OF INVENTION: Preparation of a Multicombinatorial Library of Antibody
TITLE OF INVENTION: Gene Expression Vectors
TITLE OF INVENTION: 198,381
CURRENT APPLICATION NUMBER: US/09/101,629A
CURRENT APPLICATION NUMBER: DCT/FR96/01938
FRIOR FILING DATE: 1996-12-04
FRIOR FILING DATE: 1995-12-04
NUMBER OF SEQ ID NOS: 36
SSQ ID NO 7
LENGTH: 26
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APPLICANT: Sodoyer, Regis
APPLICANT: Aujame, Luc
APPLICANT: Geoffroy, Frederique
APPLICANT: Bouchardon, Annabelle
TITLE OF INVENTION: Preparation of a Multicombinatorial Library of Antibody
TITLE REFERENCE: 98.381
CURRENT APPLICATION NUMBER: US/09/101,629A
CURRENT FILING DATE: 1999-01-12
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Pred. No.
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Patent No. 6174708
                TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 31: SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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1 Similarity 100.0%; P:
21; Conservative 0;
TELECOMMUNICATION INFORMATION:
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
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MOLECULE TYPE: CDNA
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Best Local Similarity
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Matches 21; Conserv
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US-09-101-629A-8/c
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Matches
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GENERAL INFORMATION:
APPLICANT: SODOYER, ET AL
APPLICANT: SODOYER, ET AL
APPLICANT: SODOYER, ET AL
APPLICANT: SODOYER, ET AL
TITLE OF INVENTION: EXPRESSING ANTHODY GENES
FILE REFERENCE: P03144USO/BAS
FILE REFERENCE: P03144USO/BAS
CURRENT APPLICATION NUMBER: US/08/693,234
CURRENT APPLICATION NUMBER: PCT/FR95/00127
PRIOR FILING DATE: 1996-10-04
PRIOR FILING DATE: 1994-02-10
NUMBER OF SEQ 1D NOS: 31
SOFTWARE: PAUGHT VERSION 3.1
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PRIOR APPLICATION NUMBER: PCT/FR96/0193
PRIOR FILING DATE: 1996-12-04
PRIOR APPLICATION NUMBER: FR 95 14 325
PRIOR FILING DATE: 1995-12-04
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTIN VEY. 2.1
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US-08-693-234-5
F. Sequence 5, Application US/08693234
Patent No. 6599697
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Best Local Similarity 100.0%;

Matches 21; Conservative 0
                                                                                                                                                                               TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 21; Conservative
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US-08-693-234-5
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Title: Perfect score:

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Run

Scoring table:

Searched:

Database

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Photorhabdus luminescens
Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.

CE 1 (bases 1 to 427)

RS ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
LA Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)

E 20378633

D 10919786
AQ990174 RFC00899
AQ991338 RFC00255
AQ99138 RFC00255
AQ991058 RFC01296
AQ9901031 RFC01299
AQ9901031 RFC01299
AQ9901031 RFC01299
AQ991011 RFC01864
AQ991211 RFC0132
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AQ99179 RFC02368F
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BX362060 BX362060
AL549604 AL549604
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Rfc00900 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00900, genomic survey
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
             AQ991338
AQ989502
AQ991578
AQ990513
AQ990758
AQ9901011
AQ990864
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AQ991039
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BX362060
AL549604
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AQ991774
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AQ990175
LOCUS
DEFINITION
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VERSION
KEYWORDS
SOURCE
ORGANISM
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MEDLINE
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AQ990483 Rfc01260
AQ990485 Rfc01263
AQ990287 Rfc01035
                                                                          9, 2004, 17:30:16; Search time 169.634 Seconds (without alignments) 3696.811 Million cell updates/sec
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                                                                                                                                                                                                                          55026578
            GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                    27513289 segs, 14931090276 residues
                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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                                                       sw model
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AQ990483
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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em_estro:*
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No. Result

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Gaps

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GSS 14-AUG-2000

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1 (bases 1 to 469)
Liferach-Constant, F.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                  /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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Enterobacteriaceae; Photorhabdus.
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RFC01263 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01263, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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/mol_type="genomic DNA"
/strain="W14"
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100.0%; Pred. No. 5.5e+02;
iive 0; Mismatches 0;
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Pred. No. 5.6e+02;
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Department of Biology and Biochemistry
University of Bath
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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/clone="PLG01263"
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AQ990485.1 GI:9649079
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ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, P.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 82621

Fax: (44) 1225 826779

Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTX and mapping to B.
                    This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli KI2 genome) please see ffrench-Constant et al. 2000, Nucleic
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Enterobacteriaceae, Photorhabdus.
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Rfc01260 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01260, genomic survey
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/clone="ptG01260"
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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/clone_lib="Photorhabdus luminescens strain W14 M13
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"mol type="genomic DNA"
strain="W14"
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/strain="W14"
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/clone="PLG00900"
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Class: shotgun.
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Location/Qualifiers
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  Email: bssrfc@bath.ac.uk
                                                                                                         Seq primer: M13 Forward
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AQ990483.1 GI:9649077
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Matches 21; Conservative
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Photorhabdus luminescens
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Class: shotgun.
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Rfc00899 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00899, genomic survey
   GSS 14-AUG-2000
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A genomic sample sequence of the entomopathogenic bacterium Photornabdus luminescens W14: potential implications for virulence 20378633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: bssrfc@bath.ac.uk
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annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Enterobacteriaceae; Photorhabdus.
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AQ990287

Rfc01035 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01035, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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/mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                           Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Ballding, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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1 (bases 1 to 519)
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AQ990174.1 GI:9648768
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                                                                                                                                                                           South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Faxil: bssrfcobath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTX and mapping to E.
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11 (44) 1225 826621
Fax: (44) 1225 826621
Email: bssrfc@bath.ac.uk
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
This ation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Enterobacteriaceae, Photorhabdus.
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Photorhabdus luminescens genomic clone PLG02255, genomic survey
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/clone="pLG00899"
/dev_stage="ppimary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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Environ. Microbiol. 66 (8), 3310-3329 (2000)
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1. 519
/ organism="Photorhabdus luminescens"
/mol type="genomic DNA"
/strain="W14"
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Department of Biology and Biochemistry
University of Bath
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Department of Biology and Biochemistry
University of Bath
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AQ991068 618 bp DNA linear GSS 14-AUG-2000 Rfc01926 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01926, genomic survey
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A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Enterobacteriaceae, Photorhabdus.
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Photorhabdus luminescens genomic clone PLG02569, genomic survey
Gaps
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/clone_lib="Photorhabdus luminescens strain W14 M13
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/mol_type="genomic DNA"
/strain="W14"
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100.0%; Pred. No. 5.2e+02;
iive 0; Mismatches 0;
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Department of Biology and Biochemistry
University of Bath
Mismatches
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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/clone="PLG02569"
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Photorhabdus luminescens
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                                                                                                                                                                                                      /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2.122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
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Enterobacteriaceae; Photorhabdus.
1 (bases 1 to 572)
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Rfc00051 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00051, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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/clone_lib="Photorhabdus luminescens strain W14 M13
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Pred. No. 5.2e+02;
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[mol_type="genomic DNA"
/strain="W14"
                                        'organism="Photorhabdus luminescens"
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Department of Biology and Biochemistry
University of Bath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="Genomic DNA from kb) and then الم
                                                       /mol_type="genomic DNA"
/strain="W14"
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'clone="PLG00051"
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us-10-082-772b-1.rst

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/db_xref="taxon:29488"
/clone="PLG01579"
                                                                                                        Acids Res. Seq primer: M13 Forward Class: shotgun.
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Class: shotgun.
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AQ990758.1 GI:9649352
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A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence 20378633
                                                                          1 (bases 1 to 618)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                                                                                                                                                                                  Email: bssrfc@bath.ac.uk
This is one of 2.122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
                Photorhabdus luminescens
Bacteria; Proteobacteria, Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Rfc01299 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01299, genomic survey
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/clone lib="Photorhabdus luminescens strain W14 M13
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    . .618
/organism="Photorhabdus luminescens"

                                                                                                                                                                                                                            Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
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/strain="W14"
/db xref="taxon:29488"
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Class: shotgun.
Location/Qualifiers
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AQ990513.1 GI:9649107
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nes 21; Conservative
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AUTHORS
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
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This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Photorhabdus luminescens
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Rfc01579 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01579, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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/organism="Photorhabdus luminescens"
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/clone="PLG01299"
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/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
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GSS 14-AUG-2000

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1 (bases 1 to 672)

Efrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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I (bases I to 67.8.)

I french-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
                                                                                                                                                                                                                                         Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
                                              AQ990864 linear GSS 14-AUG-:
Rfc01701 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01701, genomic survey
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Rfc02132 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02132, genomic survey
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/clone lib="Photorhabdus luminescens strain W14 M13
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/organism="Photorhabdus luminescens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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/strain="W14"
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/clone="PLG01701"
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                                                                                                                                                                                               Photorhabdus luminescens
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Class: shotgun.
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1 (bases 1 to 64)

ffrench-Constant, M.H., Waterfield, N., Burland, V., Perna, N.T.,

ffrench-Constant, M.H., Waterfield, N., Burland, V., Perna, N.T.,

A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence 20378633
                                                               /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bssrfc@bath.ac.uk
his is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to B.
coll K12 genome please see ffrench-Constant et al. 2000, Nucleic
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Rfc01864 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01864, genomic survey
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/clone lib="photorhabdus luminescens strain W14 M13
/dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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Department of Biology and Biochemistry
University of Bath
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
20376633
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Department of Biology and Biochemistry
University of Bath
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
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Enterobacteriaceae; Photorhabdus.
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Rfc01894 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01894, genomic survey
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/clone lib="Photorhabdus luminescens strain W14 M13
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                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Photorhabdus luminescens"
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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Photorhabdus luminescens
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Seq primer: M13 Forward

Class: shoctyun.

Location/Qualifiers

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Location/Qualifiers

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Location/Qualifiers

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Sequence 78, Appl
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// cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-453-702B-50

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US-09-342-268-69

US-09-3186-69

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US-09-08-11-10

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### 17-4850-779  134-7-850-779  244-708-19  647-390-15  107-755A-1  544-332-1  370-861A-1  487-826B-13  248-3847-38  248-708-39  248-708-39  248-708-39  248-708-89  236-754-3  248-708-89  236-754-3  248-708-89  236-754-3  248-708-89  236-754-3  248-708-89  248-708-89  258-754-3  264-708-89  278-754-3  28-754-3  28-754-3  28-754-3  28-8-754-3  28-8-754-3  28-8-89  28-89	ce 8544, Applice 779, Applice 19, Applice 11, Applice 1, Applice 1, Applice 1, Applice 1, Applice 13, Applice 1,		Gaps 0
117-485D-7 114-000-2779 204-708-19 647-390-15 647-390-15 107-755A-1 310-861A-1 310-861A-1 487-826B-13 224-708-39 226-754-1 204-708-39 226-754-1 204-708-39 226-754-1 204-708-39 226-754-1 204-708-39 226-754-1 204-708-89 226-754-1 226-7	Sequents Seq		490 s
	28         40         16.5         408         4         US-09-621-976-8544           29         40         16.5         4185         4         US-09-417-485D-7           31         39.6         16.3         686         4         US-09-417-485D-7           32         39.2         16.1         3680         4         US-09-647-390-15           34         39.2         16.1         676         1         US-09-647-390-15           35         39.2         16.1         676         1         US-09-647-390-15           36         39.2         16.1         6457         2         US-09-647-390-15           36         39.2         16.1         8457         2         US-09-647-332-1           39.2         16.1         13124         US-09-344-332-1           39.2         16.1         13124         US-09-344-332-1           39.2         16.1         1117         3         US-09-247-378-33           39.2         16.1         1117         3         US-09-247-373B-33           39         16.0         1011         4         US-09-247-373B-33           41         38.8         16.0         10619         4         US-09-24	ALIGNMENTS  S-08-55-978B-78/C  Sequence 78, Application US/08556978B  Patent No. 6268169  GENERAL INFORMATION:  APPLICANT: FARRESTOCK, STEPHEN F.  TITLE OF INVENTION: NOVEL RECOMBINANTLY PR TITLE OF INVENTION: SPIDER SILK ANALOGS NUMBER OF SEQUENCES: 107  CORRESPONDENCE ADDRESS:  ADDRESSEE E. I. DU FONT DE NEMOURS AND STREET: 1007 MARKET STREET  CITY: WILMINTON STRIET: DELAWARE  COUNTRY: UNITED STATES OF AMERICA  ZIP: 19898  COMPUTER READABLE FORM:  MEDIUM TYPE: DISKETTE 3.50 INCH  COMPUTER: IBM PC COMPATIBLE  COMPUTER: IBM PC COMPATIBLE  COMPUTER: DISKETTE 3.50 INCH  MEDIUM TYPE: DISKETTE 3.50 INCH  COMPUTER: BLENGESOFT WORD FOR WINDOWS 95  SOFTWARE: DISKETTE 3.50 INCH  APPLICATION NUMBER: US/08/556,978B  FILING DATE: JUNE 15, 1993  ATTORNEY APPLICATION DATA:  APPLICATION NUMBER: 08/077,600  FILING DATE: JUND ARAMETHY  REGISTRATION NUMBER: 33,692  ATTORNEY APPLICATION NUMBER: CR-9389-A  TELEFAX: 302-773-0164  INFORMATION FOR SEQ ID NO: 78:  SEQUENCE CHARACTERISTICS:  LENGTH: 4909 base pairs  TYPE: nucleic acid  STRANDEDNESS: single  TORDCOURT TYPE: DNA (Genomic)  S-08-556-9788-78	atch 100.0%; Score 243; DB 3; cal Similarity 100.0%; Pred. No. 9.8e-45; 243; Conservative 0; Mismatches 0;

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1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 60

8

Sequence (Sequence 2 Sequence Sequence S

78.6 45.8 44.6 41.6

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5933 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5993 TITIACAGIATIATGIAGICIGIIITITIATGCAAAAICIAAITITAATATATATATATATITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6053 TAICATTTTACGTTTCTCGTTCAGCTTTTTTATACTAGTTGGCATTATAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 TAICATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTTATCAATTTGCTTGCAACGAACAACGACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/08021667A
Patent No. 5434049
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ckano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLECTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLECTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 7652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                E: Diskette - 3.50 inch, 800Kb storage Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 243; DB 1;
100.0%; Pred. No. 1e-44;
:ive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: Other nucleic acid, DESCRIPTION: synthetic recombinant plasmid
                                                                                                                                                                                                                                                                                                           SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/590,988A
FILING DATE: 19901001
                                                                                    STREET: P.O BOX 2113
STREET: FIRST WISCONSIN PLAZA
                                                                 Quarles and Brady
                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19901001
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (608) 211-9166
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7652 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 7652 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 243; Conservative
                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                              ZIP: 53701
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          circular
                                                                                                                                                         WISCONSIN
                                                                                                                                                                                U.S.A.
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                                                                                                                                      MADISON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-08-021-667A-18
                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-07-590-988A-1
                                                                                                                                                                                COUNTRY:
                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19
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                                                                                                                                                                                                                                                       2336 GCTTATCAATTTGTTGCAACGAACGGCCACTATCAGTCAAATAAAATCATTATTTGAT 2277
                                                                                2456 ITTIACAGTATTATGTGTCTGTTTTTTATGCAAAATCTAATTTAATATTTGATATTTA 2397
                                                                                                                                                           2396 TATCATTTTACGTTTCTCGTTCAGCTTTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5414 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 5355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5354 TITIACAGIALTATGIAGICIGITITITIAIGCAAAAICIAATITAATATATATIGATATITA 5295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5294 TATCATTTTACGTTTCTCGGTTCAGCTTTTTTATACTAAGGCATTATAAAAAAGCATT 5235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5234 GCTTATCAATTTGTTGCAACGAACGAACTACAGTCACTATCAGTCAAAATAAAATCATTTTTTTGAT 5175
2516 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2457
                                                                                                                                   121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAGCATTGCATTATAAAAAAGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
                                                                                                                                                                                                                          181 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 TTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAATATATTTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGGTTGGCATTATAAAAAAGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Engineered E. coli plasmid pJFK4 with V. harveyi; OTHER INFORMATION: sequences inserted US-09-630-929-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 6043;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Judith W. Zyskind
TITLE OF INVENTION: USE OF ECTOENZYMES AND SECRETED ENZYMES
TITLE OF INVENTION: TO MONITOR CELLULAR PROLIFERATION
FILE REFERENCE: ELITRA.012A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 243; DB 4;
100.0%; Pred. No. 9.9e-45;
iive 0; Mismatches 0;
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Patent No. 5227288
GENERAL INFORMATION: Frederick R.
APPLICANT: Blattner, Frederick R.
TITLE OF INVENTION: DNA Sequencing Vector with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: ELITRA.012A
CURRENT APPLICATION NUMBER: US/09/630,929
CURRENT FILING DATE: 2000-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09630929
Patent No. 6620585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5174 TTC 5172
                                                                                                                                                                                                                                                                                                                                                              2276 TTC 2274
                                                                                                                                                                                                                                                                                                                    TTC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 2
US-09-630-929-4/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 4
LENGTH: 6043
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US-07-590-988A-1
                                                                                                                                                                                                                                                                                                                    241
                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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                                                                                    셤
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-828-0300
TELEX: 202-828-0380
TELEX: 248545
INPORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 201 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.
Matches 144; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arlington
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 AATTTAATATTTTATATTTATATCATTTTACGTTTCTCGTTCAGCTTTTTATACTAAG 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 TTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 18, Application US/08410544

Patent No. 5607646

GENERAL INFORMATION:
APPLICANT: Chanco, Kazuncri
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pensylvania Ave., NW
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.3%; Score 144; DB 1; Length 20 Best Local Similarity 100.0%; Pred. No. 2.6e-23; Matches 144; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                    COMPUTE: Z0009

COMPUTE: ELDOPY disk

MEDIUM TYPE: Floppy disk

COMPUTER: IEBN PC compatible

COMPUTER: IEBN PC compatible

COMPUTER: IEBN PC compatible

COMPUTER: PatentIn Release #1.0, Version #1.25

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURSTRIATION NUMBER: US/08/021,667A

FILING DATE: 19930224

CLASSIFICATION NUMBER: 20,178

REGISTRATION NUMBER: 20,178

REGISTRATION NUMBER: 520.31930X00

TELEFRONCE/DOCKET NUMBER: 520.31930X00

TELEFRA: 202-828-0380

TELEFRA: 202-828-0380

TELEFRA: 202-828-0380

TELEFRA: 202-828-0380

TELEFRA: 201-828-0380

TELEST: SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 AAAATAAATCATTATTTGATTTC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
NUMBER OF SEQUENCES: 18
                                                                                      Washington
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                                                                                    CITY: Was
STATE: D
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160 TIGGCALTATAAAAAAGCALTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTC 219
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US-08-728-785A-18

US-08-728-785A-18

Sequence 18, Application US/08728785A

Patent No. 5817506

GENERAL INFORMATION:
APPLICANT: Kambara, Hideki

TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
SULTED 1300 NO. 5817506th Seventeenth St.
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100.0%; Pred. No. 2.6e-23;
Live 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPPRATIOS SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/08/728,785A
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,544
                                                                                                                                  FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTONNEY/AGENT INFORMATION:
NAME: TERTY, DAVIG T.
REGISTRATION NUMBER: 20,178
REGISTRATION NUMBER: 520.31930X00
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; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO: 50: US-09-453-702B-50
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APPLICATION NUMBER: US/08/486,013
                                                                                                                                                                                                                                                                                                                           Query Match
43.0%; Soc
Best Local Similarity 83.2%; Pro
Matches 119; Conservative 0;
                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
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APPLICATION NUMBER: 1
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CLASSIFICATION: 530
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US-08-486-013-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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ZIP: 53701-2113
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
COMPUTER: IBM PC compatible
OPREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Berfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION CUNKNOWN.>
PRIOR APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 59.3%; Score 144; DB 1; I Best Local Similarity 100.0%; Pred. No. 2.6e-23; Matches 144; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100 AATTTAATATTGATATTTATATCATTTTACGT
                                                                                                                                                                             REPERENCE/DOCKET NUMBER: 520.31930X00
TELECOMMUTCATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    220 AAAATAAAATCATTATTTGATTTC 243
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Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/410,544
FILING DATE: 21-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bland,
Berna, Nicole T.
Plunkett, Guy
                                                                                                                                                                                                                        TELEFAX: 703-312-bbbb
TELEFAX: 703-312-bbbb
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
screanDEDNESS: single
                                                                                                                                       NAME: Terry, David T. REGISTRATION NUMBER: 20,178
                                                                                                                                                                                                                                                                                                                     TYPE: MACHOENES: SINGLE
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                               HYPOTHETICAL: Y ANTI-SENSE: NO US-08-728-785A-18
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US-09-453-702B-50
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61 ITTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
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; Patent No. 5731149
; GENERAL INFORMATION:
; APPLICANT: Solsted, Michael E.
; APPLICANT: Ouellette, Andre J.
; TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
; TITLE OF INVENTION: of Their Use
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                            Score 104.6; DB 4; Length
Pred. No. 1.4e-14;
0; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEPAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 38584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRICR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-NAY-1992
ATTOCHAGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REPERENCE/DOCKET NUMBER: P-UC 1206
TELEPHONE: (619) 535-9001
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Matches 101; Conservative
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                                                                                                                                                                                                         Length 2408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-08-482-279-69
; Sequence 69, Application US/08482279
; Patent No. 5840498
; GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    468 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 509
                                                                                                                                                                                                                                                                                                                                                                                             202 AACAGGICACIAICAGICAAAAIAAAAICAIIAITIGAITIC 243
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,279
                                                                                                                                                                                                           Score 100.4; DB 1;
Pred. No. 9.6e-14;
0; Mismatches 1;
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION: 530
FILING DATE:
REPLICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/POCKET NUMBER: 3-UC 1206
TELECOMMULCATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                           Query Match
Best Local Similarity 99.0%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2408 base pairs TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 4370 La Jo
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
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41.3%; 99.0%;

Query Match Best Local Similarity

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                                                                                             408 CICCITITITATACTAAGTIGCCATTATAAAAAGCATIGCTTATCAATTIGTIGCAACG 467
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Gaps
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Patent No. 5844072
GABEAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCES ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.3%; Score 100.4; DB 2; Length 2408;
Indels
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                                                                                                                                                                           468 AACAGGICACIAITCAGICAAAAIAAAAICAITAITIGAITIC 509
                                                                                                                                             202 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 243
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MEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPAGISH
COMPUTER: PROPAGISH
COMPUTER: PROPAGISH
CORPAGE: PATON: 435
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,268
FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
RICASSIFICATION: 435
RICASSIFICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-ANG-1992
PRIOR APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-AMR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 9-UC 1206
TELECOMMUNICATION NUMBER: 9-UC 1206
TELECOMMUNICATION NUMBER: 9-UC 1206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score luu.:,
Pred. No. 9.6e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2408 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.0
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 92122
                                                                                                                                                                                                                                                                 RESULT 10
US-08-342-268-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
US-09-015-968-69
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408 CIGCITITITATACTAAGTIGGCATTATAAAAAAGCATIGCTIATCAATTIGTIGCAACG 467
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Patent NO. 6395963

GENERAL INFORMATION:
APPLICANT: Onl, Stephan
APPLICANT: Van Der Lee, Frederique
APPLICANT: Riap, Joke
APPLICANT: Klap, Joke
TITLE OF INVENTION: Nematode-Inducible Regulatory DNA Sequences
FILE REPERENCE: MOG 57680
CURRENT APPLICATION NUMBER: US/09/308,090
CURRENT FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 2408;
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                                                                                                                 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 100.4; DB 4.
Pred. No. 9.6e-14;
0; Mismatches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AFLILMATION NUMBER: US/09/39/,386
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
FILING DATE:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-UN-1995
FILING DATE: 07-UN-1995
FILING DATE: 108 08/482,279
FILING DATE: 108 08/482,279
FILING DATE: 108 08/482,279
FILING DATE: 14-NOV-1994
FILING DATE: 14-NOV-1994
FILING DATE: 14-NOV-1997
FILING DATE: 14-NOV-1992
FILING DATE: 126-NAX-1992
ATTORNEY APPLICATION NUMBER: US 07/899,020
FILING DATE: 26-NAX-1992
ATTORNEY APPLICATION NUMBER: 26-NAX-1992
ATTORNEY APPLICATION NUMBER: US 07/899,020
FILING DATE: 26-NAX-1992
                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PETENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-UC 3003
                                                                                   Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: P-UC
TELECOMMUNICATION INFORMATION:
TELEPRONE: (619) 535-9001
TELEPAX: (619) 535-8949
INPORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Campbell, Cathryn A. REGISTRATION NUMBER: 31,815
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.3%;
                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 101; Conservative
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                                                                                                                 STREET: 4370 La Jol
CITY: San Diego
STATE: California
COUNTRY: USA
                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
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US-09-397-386-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
US-09-308-090-1
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Sequence 69, Application US/09015968
Patent No. 6057425
Patent No. 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-09-397-386-69
is Gquence 69, Application US/09397386
j Fatent No. 6300470
j GENERAL INFORMATION:
j APPLICANT: Selsted, Michael E.
j APPLICANT: Ouellette, Andre J.
j TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
j TITLE OF INVENTION: of Their Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           202 AACAGGICACTAICAGICAAAAIAAAAICAITAITIGAITIC 243
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                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
STATE: Can Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHAK: (619) 535-9949
INFORMATION FOR SEQ ID NO: 69.
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
FILING DATE:
CLASSIFICATION:
PRIOR PAPLICATION DATA:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-UN-1995
RICR APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
FILING DATE: 14-NOV-1994
PRIOR APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-NG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 26-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: CAMPDELICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: CAMPDELICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-09-015-968-69
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420 CTGCTTTTTTTTTTTATACTTGCCATTATAAAAAGCATTGCTTGTTGCAACG 479
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                                                                                                                                                                                                                                                                                                                                                                               41.3%; Score 100.4; DB 4; Length 3484; 99.0%; Pred. No. 9.9e-14; cive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 AACAGGICACIAICAGICAAAAIAAAAICAIIAIIIGAIIIC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 13, Application US/09016366A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: INHIBITORS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           UMDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastENG for windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPTICATION: 530
                                                                                                                                                                                                                                       NAME/KEY: CDS
LOCATION: 3481.3484
CTHER INFORMATION: /codon_start= 3482
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                  ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B0801/7093
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APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
    TYPE: nucleic acid
STRANDENBESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Plumer, Elizabeth R. REGISTRATION NUMBER: 36,637 REFERENCE/DOCKET NUMBER: BO TELECOMMUNICATION INFORMATION: TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13:
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3757 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                              HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                           STRAIN: C24
                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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US-09-016-366A-13
                                                                                                                                                                                                                   FEATURE
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STATE:
                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                           Length 3484;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: INAMP. 1999
CLIASSIFICATION NUMBER: US/09/380,090A
FILING DATE: IN-May-1999
CLASSIFICATION NUMBER: WO PCT/EP97/06472
FILING DATE: I8-NOV-1997
APPLICATION NUMBER: BP 96203213.2
FILING DATE: IB-NOV-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GODDIJN, Oscar
KLAP, Joke
TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA
SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               202 AACAGGICACIAICAGICAAAAIAAAAICAIIATIIGAIIIC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          480 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 521
                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                                                                                                                                                                                                      Query Match 41.3%; Score 100.4; DB 4 Best Local Similarity 99.0%; Pred. No. 9.9e-14; Matches 101; Conservative 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application US/09380090A
Patent No. 6555529
GENERAL INFORMATION: Stephan Andreas
APPLICANT: OHL, Stephan Andreas
KLEIN-VAN DER LEE, Frederique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: SYN-010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
TELEPAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
EARLIER APPLICATION NUMBER: PCT/EP97/06472
EARLIER FILING DATE: 1997-11-18
EARLIER APPLICATION NUMBER: EP 96203213.2
EARLIER FILING DATE: 1996-11-18
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 3484
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ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
CITY: Boston
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REGISTRATION NUMBER: 39,850
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COUNTRY: United States
                                                                                                                                                                                           TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: (3482)..(3484)
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US-09-380-090A-1
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US-09-016-366A-13

0; Query Match 41.3%; Score 100.4; DB 2; Length 3757; Best Local Similarity 99.0%; Pred. No. 9.9e-14; Matches 101; Conservative 0; Mismatches 1; Indels 0; Gaps

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Search completed: September 9, 2004, 21:21:18 Job time : 55.5798 secs

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September 9, 2004, 15:48:15 ; Search time 1677.36 Seconds
(without alignments)
6279.120 Million cell updates/sec
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243
1 tctgttacaggtcactaata......taaaatcattatttgatttc 243
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            3470272 segs, 21671516995 residues
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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PAT 21-MAR-2001					oviridae;					
PAT					; Siph				cells	
linear					Caudovirales				eukaryotic	
DNA					age;				ni no.	1,
AX092113 243 bp	Sequence 2 from Patent WO0116345. AX092113	AX092113.1 GI:13444356	Bacteriophage lambda	Bacteriophage lambda	Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;	Lambda-like viruses.		Droege, P.	Sequence-specific dna recombination in eukaryotic cells	Patent: WO 0116345-A 2 08-MAR-2001;
RESULT 1 AX092113 LOCUS AX	DEFINITION SE ACCESSION AX	VERSION AX KEYWORDS .	SOURCE Ba	ORGANISM Ba	Vi	La	REFERENCE 1	AUTHORS Dr	TITLE Se	JOURNAL PA

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Warayrota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, lamiids, Bolanales, Solanaceae, Nicotiana.
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Macaca fascicularis (crab-eating macaque)
Macaca fascicularis
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
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                                       GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                    TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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100.0%; Pred. No. 7.3e-34;
ive 0; Mismatches 0;
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    .610
    /organism="Nicotiana tabacum"
/mol_typis="unassigned DNA"
/db_xref="taxon.6097"

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Patent: WO 0121780-A 1 29-MAR-2001;
THE UNIVERSITY OF LEEDS (GB)
                                                                                                                                                                                                                                                                                                      Nicotiana tabacum (common tobacco)
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Sequence 1 from Patent WO0121780.
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Matches 243; Conservative
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site-specific recombination.
Bacteriophage lambda
Bacteriophage lambda
Bacteriophage lambda
Viruses; dsDNA viruses.
1 (bases 1 to 361)
Schmeissner, U., McKenney, K., Rosenberg, M. and Court, D.
Removal of a terminator structure by RNA processing regulates int
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                                                 /organism="Bacteriophage lambda"
/mol_type="unassigned DNA"
/db_xref="taxon:10710"
                                                                                                                                   ; Score 243; DB 6;
; Pred. No. 8.9e-34;
0; Mismatches 0;
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/db_xref="taxon:10710"
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Original source text: P.falciparum, cDNA to mRNA, clone M4 Location/Qualifiers
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Key Location/Qualifiers
misc feature (1): (1763).
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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SGTYNKLIETLCLIHSNGDPKWIQSVPIWERSPWVETEMGYKKLLSEEEGPRLESSHLPI
OFTPKSFFSKAKVIYLMRNPRDVFVSCYFFWNSVKFVKKRKRWQQYFEWFCGGNUIY
GSWFDHIHGMMPMREKKUFLLISYEELKQDFRRTYDEKICQFIGKTLEPEELNIILKNS
SFQSMKENKMSNFSLLSVDFVEEKAQLLRKGISGDWRNHLTVAQAEAFDKLFQEKTUD
                                                                       Ogura.K.
Direct Submission

Direct Submission

Submitted (13-MAY-1996) Kenichiro Ogura, Tokyo University of Submitted (13-MAY-1996) Kenichiro Ogura, Tokyo University of Submitted and Life Science, Department of Drug Metabolism and Molecular Toxicology; 1432-1 Horinouchi, Hachioji, Tokyo 192-0392, Japan (E-mail:ogurak@ps.toyaku.ac.jp, Tel:+81-426-76-4518, Fax:+81-426-76-4517)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae;
           Ogura,K., Satsukawa,M., Kato,K., Okuda,H. and Watabe,T.
Molecular cloning of monkey liver hydroxysteroid sulfotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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Worley, P.F., Lanahan, A., Goetz, B., Hiemisch, H., Kuner, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 243; DB 9; Length 1668;
Pred. No. 6e-34;
Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA linear for using the same.
                                                                                                                                                                                                                        /organism="Macaca fascicularis"
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|clone="monHST-1"
                                                                                                                                                                                                                                                                                                                                                                         /product="hydroxysteroid
/protein_id="BAA12823.1"
                                                                                                                                                                                                                                                                                                        tissue type="liver"
clone_lib="lambda gt11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BD225932 1763 bp
Immediate early gene and method
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BD225932.1 GI:33035702
BD2202512772-A/49.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="GI:1345406"
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100.0%; Pre
tive 0; h
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(bases 1 to 1668)
                                                             (bases 1 to 1668)
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Best Local Similarity
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BD225932/c
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OS Rattus norvegicus (rat)

PN JP 2002512772-A/49

PD 08-MAY-2002

PP 08-MAY-2002

PF 05-FEB-1999 UP 2000530634

PR 09-FEB-1999 UP 2000530634

PRUDL F WORLEY, ANTHONY LANAHAN, BERNARD GOETZ, HOLGER HIEMISCH, PI ROHINI KUDER,

PAUL F WORLEY, ANTHONY LANAHAN, BERNARD GOETZ, HOLGER HIEMISCH, PI ROHINI KUDER,

PAUL F WORLEY, ANTHONY LANAHAN, BERNARD GOETZ, HOLGER HIEMISCH, PI ROHINI SCHEEK, KAROLY NIKOLICH, EUGENE ZHUKOVSKI PC C12N15/09, A61K31/711, A61K48/00, A61P25/00, A61P25/28, C07H21/04, PC C07K16/18, G101N33/53,

PC C12N15/09, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12P21/08 PC C12N15/00, C12N5/00

CC n is either a, t, g, or c FH Key Location/Qualifiers

FT misc_feature (1) (1763).
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Plasmodium falciparum (malaria parasite P. falciparum)
Plasmodium falciparum (malaria parasite P. falciparum)
Blasmodium falciparum
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
Scheek, S., Nikolich, K. and Zhukovski, E.
Immediate early gene and method for using the same
Patent: JP 2002512772-A, 49 0B-MAY-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE, BASF LYNX
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2369

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THYVKNUKHKEYPAFHILARLMNAHPERMAMATOGELVIMBSVHACYTYFHEQTETF
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ANMDNFFAPVFTYGGBKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                                                                                                                                   SYN 20-JUL-2000
                                                                                                                                    2368 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAATAAAATCATTATTTGAT 2309
                                                                                                                                                                                                                                                                                                                   AF178449 3485 bp DNA linear SYN 20-JUL-2(
Integration vector pCD11PKS chloramphenicol transacetylase (cat)
and beta-galactosidase alpha peptide (lacza) genes, complete cds.
AF178449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="attp; attachment site from bacteriophage lambda"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 3485),
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and
lacZ gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
                         2428 TAICATTTTAGGTTTCTGGTTCAGCTTTTTTTATACTAAGTTGGCATTATAAAAAAAGCATT
                                                                                           GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
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1. .385
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Integration vector pCD11PKS
artificial sequences; vectors.
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/transl_table=11
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DDQDYCTCTRRTIYESMDNTVEFAKKMYELSA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /trānslation="MYLFIYIFFFFFFFFFVIVQKDIEQLDIKCAHEQMNIQKQYDE
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DNEIPKWSIPEWFTTDELQDKPDVGELIRREIWHNPLSYYLGLEEFDEFDDFPEEFD
DDDDDDDDDDDDDDDDDKDDLDGDDGNNDDNDD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MVLVTCNRALAQGDFCLLALIFCHQTCRTPEKHKASQSSAKLVS
INISLITSHHRLRHPRRRQHHRNNFAPTNWYWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2488 ITTTACAGTATTATGTAGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTTGTATTTA 2429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="PQYQFVGAKLFRWWCWRRRGWRRRWWLVIKLMLIETSFALDCEA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2548 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (2141. .2650)
/note="putative VECTOR sequence Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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protein_id="AAA29621.1"
db_xref="G1:160343"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="histidine rich protein D"
protein_id="AAA29622.1"
db_xref="G1:160344"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ដ
                                                                                                                                                                             protein A"
/organism="Plasmodium falciparum"
/mol type="genomic DNA"
/db_xref="taxon:5833"
1. .234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="histidine rich protein
protein id="AAA29620.1"
'db_xref="GI:160342"
                                                                                                                                                                                                                                                                                       824. .1072
Gene="histidine rich protein B"
824. .1072
/gene="histidine rich protein B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement (828. .1589)

Gene="histidine rich protein B"
complement (828. .1589)
/gene="histidine rich protein B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1525. .>2758
/gene="histidine rich protein C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 243; DB 3;
100.0%; Pred. No. 5.4e-34;
ive 0; Mismatches 0;
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                                                                                                                                    gene="histidine rich protein A"
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/gene="histidine rich protein C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(2596. .2758)
/gene="histidine rich protein D"
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                                                                                           gene="histidine rich protein
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                                                                                                                                                             codon_start=1
product="histidine rich
                                                                                                                                                                                                 /protein_id="AAA29618.1"
/db_xref="G1:160340"
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Best Local Simil
Matches 243;
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ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                                      /trānslation="mtmltpsaqitltkgnksmsstavaaaleludppgcrnslssls
ipstsrggpvpnspysesyyarslavvliqrrdmenpgvtqlnrlaahpppaswrnsee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="aminoglycoside 3' phosphotransferase"
/protein id="AAF82363.1"
/db xref="G1:9022392"
/translation="WSHIQRETSCSRPRINSNMDADLYGYKWARDNVGQSGATIYRLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  circular SYN 11-JUL-2000
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statisficial sequences; vectors.

1 (bases 1 to 4105)
Wiencis,A.M., Keagle,P., Andersen,J., Wotanis,J., Newcombe,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (24-MAY-2000) Molecular Genomics, Aventis
Pharmaceuticals, 26 Landsdowne Street, Cambridge, MA 02139, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITIACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAAITIAAAIAIATIGAIAIIIAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                             Length 3485;
                                                                                                                                                        /transT_table=11
/product="beta-galactosidase alpha peptide"
/protein id="AF86672.1"
/db_xref="G1:9294789"
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function="confers kanamycin resistance"
                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 243; DB 12; 100.0%; Pred. No. 5.2e-34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .4105
/organism="Cloning vector pLDR9"
/mol_type="genomic DNA"
/db_xref="taxon:130501"
216. .1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete sequence.
                                                                                                                                                                                                                                                                                             2972. .3081
/note="multiple cloning site"
                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                               ARTDRPSQQLRSLNGEWLTRPVAAH"
                                                                                              .3137)
                                                           complement (2754. .3137)
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                                                                                              complement (2754.
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/transl_table=11
                                                                                                                                     /codon_start=1
/transl_table=
                                                                                                                   /gene="lacza"
                                                                                  /gene="lacza"
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AF271663
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                                                                                                                                                                                                                                                                                                                                                                                                                     243; Conservative
                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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VERSION
KEYWORDS
                                                             gene
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JOURNAL
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AF271663
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LKTVKKNKHKFYPAFIHILARLMNAHPEFRMAMKDGELVIWDSVHPCYTVFHEQTETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           668. .915
/note="attP; attachment site from bacteriophage lambda"
complement(1327. .1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          artificial sequences; vectors.

1 (bases 1 to 3485)
Platt, F., Drescher, C., Park, S.K. and Phillips, G.J.
Genetic system for reversible integration of DNA constructs and lacZ gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
                                                                                                                                                          TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                     ;
0
                                                                            Length 3485;
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                                                                                                                     Indels
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/organism="Integration vector pcDllPSK"
/mol_type="genomic DNA"
/db xref="taxon:106603"
/lab_host="Escherichia coli"
1. .385
                                                                            100.0%; Score 243; DB 12;
100.0%; Pred. No. 5.2e-34;
tive 0; Mismatches 0;
2972. .3081
/note="multiple cloning site"
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/product="chloramphenicol
/protein_id="AAF86673.1"
/db_xref="G1:9294790"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (1327. .1986)
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Integration vector pCD11PSK
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                                                                                                                   Conservative
                                                             Query Match
Best Local Similarity
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AUTHORS
TITLE
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LRGALDAGGRIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="plasmid origin of replication; base 1653 represents
the first base of the newly synthesized strand"
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/note="Multiple Cloning Site (MCS); contains unique sites for Sfil, Xhol. EcoRl, BamHI, Not!, Mlul, HindIII" complement (2155. 2174)

/gene="T7 RNA polymerase" complement (2155. 2174)

/gene="T7 RNA polymerase"
                   Submitted (19-AUG-1994) James A. Malone, International Technical Submitted (19-AUG-1994) James A. Malone, International Technical Services, Molecular Biology Reagents Division, Pharmacia Biotech Inc., 2202 N. Bartlett Ave., Milwaukee, WI 53202-1009, USA Location/Qualifiers
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production of single-stranded DNA; base 2933 represents
the first base of the newly synthesized single strand"
                                                                                                                                                                                                             /organism="unidentified cloning vector"
|mol_type="genomic DNA"
|mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="attP gene from lambda"
3932. .3947
/gene="attP"
/note="att core"
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/gene="SP6 RNA polymerase"
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'gene="SP6 RNA polymerase"
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/gene≂"lac"
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/gene="lac"
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/gene="bla"
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PExcell. A multifunctional cloning vector that is released from lambda Excell by in vivo excision Unpublished (1994).
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T7 promoter; SP6 promoter; beta-lactamase, lacZ alpha peptide,
attP.
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/note="hypothetical 9.2 kD protein"
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iive 0; Mismatches 0;
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                                                                                                                                                       /EC_number="3.5.2.6"
/note="derived from pMMB66EH"
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unidentified cloning vector
artificial sequences; vectors.
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product="unknown"
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/codon_start=1
/transl_table=11
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/db_xref="101:924795"
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AF178453
Integration vector pCD13PSX aminoglycoside adenyltransferase (aada) and beta-galactosidase alpha peptide (lacZa) genes, complete cds. AF178453
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Platt, R., Drescher, C., Park, S.K. and Phillips, G.J.
Direct Submission
Submitted (18-AUG-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
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Integration vector pCD13PSK
artificial sequences; vectors.

1 (Dases 1 to 4549)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and lacZ gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
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    4549
    /organism="Integration vector pCD13PSK"

                                                                                                                                                                                                                                                                                                                                      100.0%; Score 243; DB 12;
llarity 100.0%; Pred. No. 4.9e-34;
Conservative 0; Mismatches 0;
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/note="multiple cloning site"
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/db_xref="taxon:106606"
/lab_host="Escherichia c
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                                                             /gene="lacza"
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/db_xxef="G1:9294796"

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VTGKIAPKDVAADWAAMERLPAQYQPVILEARQAYLGQEEDRLASRADQLEEFVHYVKG
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complement(1798, .2652)
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Platt, K., Drescher, C., Park, S.K. and Phillips, G.J.
Genetic system for reversible integration of DNA constructs and lacz gene fusions into the Bscherichia coli chromosome
                                                                                                               TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                       1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                        TTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
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, Score 243, DB 12, Length 4190;
, Pred. No. 5e-34;
0; Mismatches 0; Indels 0;
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
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/mol_type="genomic DNA"
/db_xref="taxon:106605"
/lab_host="Escherichia coli"
1. 385
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Integration vector pCD13PKS
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100.0%; Pred. No. 4.7e-34;
ative 0; Mismatches 0;
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Patent: WO 0127322-A 14 19-APR-2001,
Elitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
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                                                                    /note="pJMF3"
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Matches 243; Conservative
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VTGKIAPKDVAADWAMBRLPAQYQPVILEARQAYLGQEBDRLASRADQLEEFVHYVKG
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complement(1798. .2652)
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                                                                               /codon start=1
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100.0%; Pred. No. 4.9e-34;
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Chitobiase as a reporter enzyme
Patent: WO 0127322-A 13 19-APR-2001;
Blitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
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complement(3818. .4201)
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Chitobiase as a reporter enzyme
Patent: WO 0127322-A 11 19-APR-2001;
Blitra Pharmaceuticals, Inc. (US)
Location/Qualifiers
1. 5826
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/db_xref="taxon:32630"
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                                                                                                      DNA
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Sequence 11 from Patent WO0127322.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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genesegn1990s:*
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                                                                             - nucleic search, using
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Maximum DB seq length: 2000000000
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Match Length
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Aac5525 Donor pla Aac5526 Donor pla Aac5532 Donor pla Abc5876 Donor pla Abc5876 Donor pla Abc82130 Acceptor Abc82130 Acceptor Aac55382 Recombina Aac5532 Donor pla Aac5522 Donor pla Abc5876 Destinati Abc5876 Denor pla Aac55525 Donor pla Aac55526 Donor pla Aac55632 Donor pla Aac55632 Donor pla Aac55632 Donor pla Aac55636 Donor pla	NTS		integrase; gene therapy; somatic;	in eu integ	a novel sequence-specific recombination (SSR) of a novel sequence-specific recombination (SSR) of an integrase (Int) to effect SSR. The invention cleic acid comprising a 243 base pair sequence the specification, or its derivatives; and (2) to rise derivatives, plus a therapeutic gene, or thod is particularly used in somatic gene therapy but can be applied more generally for gene therapy but can be applied more generally for gene therapy but can be applied more generally for gene therapy but can be applied more generally for gene therapy but calls. The method is simple and controllable, targeted integration of selected DNA sequences
AAC55525 AAC55526 ABC5532 ABC5130 ABC82130 AAC55523 AAC55523 AAC55523 AAC55523 AAC55523 AAC55523 AAC55523 AAC55523 AAC55523 AAC55525 AAC55525 AAC55525 AAC55526 AAC55526 AAC55526 AAC55526	ALIGNMENTS BP.	A fragment	s.	ion of DNA Y, uses an	a novel sequence in comprising introverse (Int) leic acid comprise the specification or its derivative hod is particular ut can be applied ant celle. The metargeted integrat
	243 E	r) DNA	9 9	mbinatio: therapy,	s a na 1, con cleic cleic the thod thod but c
4939 51156 55184 55884 108691 2333 2333 44208 44470 44470 4627 4627 4627 4639 5584 5584 5156 5156 5156	DNA;	st entry) bda attP	ic recombina ation; attP; ambda.  99DE-0104118	recomb recomb gene th	describes a nyterior cell, colly using an in (1) a nucleic efined in the infill, or s. The method animals, but chable and targtable and targtable cells.
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                                                                                                                    GCTTATCAATTTGTTGCAACGGAACAGGTCACTATCAGTCAAAAATAAAATCATTATTTGAT
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                        Score 243; DB 8;
Pred. No. 1.8e-40;
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                                                        Mismatches
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Matches 243; Conservative
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Shellard
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for the site-specific integration of a DNA sequence into the plastid DNA of a plant or its derived cells. Transgenic plants in which a DNA sequence has been integrated, also their cell cultures, organs, tissues etc. are useful in human or animal nutrition, to produce seeds, and to produce pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids, flavourings and aromatizing agents, dyes, antibodies and vaccines. The present sequence is a recognition sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site-specific integration of DNA into plastid DNA, useful for making transgenic plants used e.g. as food, by recombinase-mediated insertion.
                                                                                                                         TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                        Gaps
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                                   Length 243;
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74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;
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0
                               Score 243; DB 4;
Pred. No. 1.8e-40;
                                                                   0; Mismatches
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                                                                    Conservative
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                                                 Similarity
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 Sequence 243
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one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (1) a platform artificial chromosome expression system (ACes) (11) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial

Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;

The present invention describes a eukaryotic chromosome (1) comprising

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chromosome. (I) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform attificial chromosome, preferably an Aces. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic
                                                                                                                                                                                                                                                                                            o;
                                                                                                                  cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
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, Pred. No. 1.8e-40;
0; Mismatches 0; Indels (
                                                                                                                                                                                                                        Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
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                                                                                                                                                                                        exemplification of the present invention
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chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes oselected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, KNA, KNA, structural proteins, marker proteins, ligands, receptors, iboozymes, therapeutic proteins, and proteins, antisense RNA, trons, structural proteins, and proteins, antisense provents, antisense, horodicated actors, antisense, horodicated actors, antisense, horodicated actors, antisense, in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (RAC). This producing plant artificial chromosomes of the invention
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Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74
                                                                                                                      The invention relates to a novel method for producing plant artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAATATATTGATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       135 TATCATTTTACGTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rcrerracagercacraaraccarcraagergricaracaracracaratere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Attachment P region; attP; recombination; marker gene removal; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 243; DB 7;
100.0%; Pred. No. 1.8e-40;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage lambda attachment P region.
                                                                               Disclosure; Page 263-264; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-SEP-2000; 2000WO-GB003543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF79770 standard; DNA; 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 100.
Matches 243; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15
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The sequences given in ABQ80104-05 are primers which were used to amplify DNA for use in the material of the invention. The primers amplify a 1377 DNA for use in the material of the invention. The printion of lambda phage DNA contained in a plasmid. The amplified sequence (ABQ80306) was attached to the printer material of the invention which comprises at least one support having at least one oligomer and/or contained on it. The printed material is useful in a method for synthesising DNA where the product of amplification and/or ligation is contained on it insertion/deletion, single nucleotide contained insertion/deletion, or SNP andlysis. Continually, the CNA and/or full-length CDNA is useful for the peptide or protein expression. The printed material is useful in research applications, or for providing scientists with oligomer and/or polymers from the printed materials alless and/or polymer can be obtained immediately and directly, without need to make a request for it. The coligomers and/or polymers and/or polymers can be delivered and stored easily with reduced labour and time while eliminating the need to use special equipment or the contained are and the printed material is a safety and directly, without need to make a request for it. The coligomer and time while eliminating the need to use special equipment or the coligomer and time while eliminating the need to use special equipment or the coligomer and time while eliminating the need to make a request for it.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 TITIACAGIATIAIGIAGICIGIITITIAIGCAAAAICIAAITIAAIAIATIGAIAITIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     808 renginacaggicaeranacareraagnagngaricaragigaergearanging
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           928 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAGCTTGGCATTATAAAAAGCATT
                                                                                                                                                            Printed material useful as a delivery and storage system for oligomer and/or polymer, comprises a support having an oligomer and/or polymer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   868 TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           facilities. Thus, the printed material is a quick, efficient and inexpensive sample delivery system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriophage lambda DNA, SEQ ID NO:3 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 243; DB 7; 100.0%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                             Example 1; Page 31-32; 91pp; English.
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                                                    Hayashizaki Y;
(RIKE ) RIKEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27-AUG-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes a method of removing a transgene marker by flanking the transgene with a bacteriophage lambda attachment P (attP) region and inducing homologous recombination between attP regions so that the transgene is removed. This is useful in the production of transgenic plants with less risk of inter-species transmission of marker genes, which often encode proteins associated with, for example, herbicide and antibbotic resistance. The present sequence is the attP coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198
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                                                                                                                                                                                                                      Removing a part of a transgene which has been integrated into a genome comprises inducing intrachromosomal homologous recombination between the attachment P regions of bacteriophage lambda flanking the transgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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deletion; single nucleotide polymorphism; sequencing; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 243; DB 5; 100.0%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                   Claim 8; Fig 3D; 25pp; English.
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  99GB-00021937.
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1es 243; Conservative
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                                                                                                             Zubko E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTC 243
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  17-SEP-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                             oligomer and/or polymer applied on support. The support has oligomer and/or polymer applied on it, and is in the form of loose-leaf sheet or card. The support is useful for storing and/or delivering an oligomer and/or polymer applied on it. The present sequence is Bacteriophage lambda DNA used in the exemplification of the invention
                                                                                                                                                                                                                                                                                New support useful for storing and/or delivering an oligomer and/or polymer applied on support, has oligomer and/or polymer applied on it, and a loose-leaf sheet or a card.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       808 rererracadereacranaraceareragradizarrearagraerecararere
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immediate early gene; IEG; neuron; brain; function; growth factor;
transcription factor; signal transduction; cytoskeletal protein;
metabolic enryme; learning; memory; synaptic transmission; tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a method for storing and/or delivering an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 243; DB 7; Length 1469; 100.0%; Pred. No. 1.9e-40; ive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat neuronal immediate early gene cDNA clone R280.
                                                                                                                                                                                                                                                                                                                                             Example 1; Page 30-31; 70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ30709/c
ID AAZ30709 standard; cDNA; 1763
                                                                                          05-NOV-2002; 2002WO-JP011492.
                                                                                                                         05-NOV-2001; 2001JP-00339217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   neuronal plasticity; ds.
                                                                                                                                                       (RIKE ) RIKEN KK.
(DNAF-) DNAFORM KK.
(HAYA/) HAYASHIZAKI Y.
                                                                                                                                                                                                                                                    WPI; 2003-441569/41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1048 TTC 1050
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                             WO2003040360-A1
                                                                                                                                                                                                                     Hayashizaki Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JAN-2000
                                                            15-MAY-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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clone R280. An IEG is a game whose expression is rapidly increased immediately following a stimulus e.g., neuronal stimulation. Such neuronal IEGs have been found to encode a variety of proteins, including transcription factors, cytoskeletal proteins, growth factors and metabolic enzymes, as well as proteins involved in signal transduction. The identification of neuronal IEGs and the proteins they encode may provide important information about the function of neurons in, for example, learning, memory, synaptic transmission, tolerance and neuronal EGS and antibodies against neuronal IEG proteins can be used to treat an animal with a deficiency in neuronal IEG responsivity to stimuli, such that the effect of the deficiency is minimised. The deficiency may be a reduced or elevated level of expression of an IEG. The neuronal stimulus comprises a maximal electroconvulsive seizure and its effects influence learning or memory. The IEGs and products are useful in identifying compounds that modulate the expression or accountly of IEG nucleic acids or proteins, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ó
                                                                                                                                                                                                                                                                                                                                      treating conditions related to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             372
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 ITTIACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              371 TITIACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAAITIAAIAIAITIGAIAITIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 TATCATTTTACGTTTCTCGTTCAGCTTTTTATACTAAGTTGGCATTATAAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence represents rat neuronal immediate early gene (IEG) cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                 Scheek S;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                               Kuner R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 243; DB 2; 100.0%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                    Novel genes and polypeptides, useful for treatir
deficiency in nIEG responsiveness to a stimulus
                                                                                                                                                                                                                                               Hiemisch H,
                                                                                                                                                                                        (UVJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE (BADI ) BASF-LYNX BIOSCIENCE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 114-115; 134pp; English.
                                                                                                                                                                                                                                               Goetz B,
                                                                                                     99WO-US002462
                                                                                                                                      98US-0074135P
98US-0074518P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 100.
Les 243; Conservative
                                                                                                                                                                                                                                               Lanahan A,
Zhukovski
                                                                                                                                                                                                                                                                                                   WPI; 1999-590697/50
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TTC 189
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                               W09940225-A1
                                                                                                     05-FEB-1999;
                                                                                                                                    09-FEB-1998;
12-FEB-1998;
                                                                                                                                                                                                                                               Worley PF, 1
Nikolich K,
                                                                  12-AUG-1999
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ACC44716 ID ACC44716 standard; DNA; 4346 BP.

RESULT 9

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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombination, and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for chromosome. (I) can be used in gene therapy. (MI) is useful for chromosome, preferably an ACes. (II) is useful for producing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4070 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAGTTGGCATTATAAAAAAGCATT 180
                                                                                                                                     Chromosome-based platform, artificial chromosome, eukaryotic chromosome, att site; integrase, recombinase, ACes, gene therapy, transgenic animal, platform artificial chromosome expression system; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fleming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                  Plasmid pSV40193attPsensePUR nucleotide sequence SEQ ID NO:113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 4346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Leung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 243; DB 7;
Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greene A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 244-245; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lindenbaum M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                              30-MAY-2002; 2002WO-US017452
                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2001; 2001US-0294758P.
                                                                                                                                                                                                                                                                                                                                                                                                                       21-MAR-2002; 2002US-0366891P.
                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perez C, Li
Shellard J;
                                                                                                                                                                                                                       Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2003-140461/13
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Best Local Similarity
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                                                          29-MAY-2003
                                                                                                                                                                                                                                                                                                                       05-DEC-2002
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Stewart S,
                                                                                                                                                                                                                                       Synthetic
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                    ACC44716;
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Matches
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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods insertion of heterologous DNA into plant artificial chromosomes. The isolated plant chromosomes one elected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product cuch as enzymes, antisense RNA, tRNA, tNNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and biopharmaceutical proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (EAC) or a yeast artificial chromosome (EAC) or a yeast artificial chromosome (EAC).
4190 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT 4249
                                                                                 4309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
                                          181 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAATAAAATCATTATTTGAT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                  4250 GCTIATCAATITGTTGCAACGAACAGGTCACTATCAGTCAAATAAAATCATTAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chromosome (BAC) or a yeast artificial chromosome (YAC). This polynucleotide sequence represents the DNA of a plasmid used in the
                                                                                                                                                                                                                                                                                                                                                                                              Artificial plant chromosome related plasmid DNA SEQ ID No 26.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 19; Page 255-256; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perkins E;
                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                        ABT16615 standard; DNA; 4346
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                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-140436/13.
                                                                                                                                                                 rrc 4312
                                                                                                                            TTC 243
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unidentified.
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Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 U; 0 Other;

Length 4346;

DB 7;

100.0%; Score 243;

Query Match

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Gaps

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coatings, etc
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21-JUN-2001
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                                                                                                                                                                                                 4250 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT 4309
                                                                TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 4129
                                                                                                                                                              TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAGGTTGGCATTATAAAAAGCATT 4249
                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents the complete nucleotide sequence of the plasmid which was used in the construction of the vector pPP510 which was used to express synthetic spider dragline variants, DP-1B.9 md DP-1B.9. ph126; comprises a replication origin active in E. coli, a selectable genetic marker which is a gene conferring resistance to ampicially, sites for the restriction endomucleases BamHI and BgIII with no essential sequences between them, and a third restriction site for PstI, located within the selectable marker which produces cohesive ends incompatible with those produced by BamHI and BgIII. The polypeptide monomers are variants based on a consensus sequence derived from the fibre forming regions of spider dragline protein, esp. the natural protein 1 (Spidroin 1) from Nephila clavibes. Synthetic analogues of DPI
                                                                                           TITIACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAAITITAAIATATIGAIATITA 120
                                                                                                                                        TAICATITIACGITICTCGTICAGCITITIATACTAAGTIGGCATTATAAAAAGCATT 180
                                                                                                                                                                                   Spider; dragline protein; variant; monomer; polymer; circular; there forming region; Spidroin 1; Nephila alavipes; DP1; mimic; DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope; surgical suture; implant; reinforcement; film; coating; ss.
                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells.
                                            TCTGTTACAGGTCACTAATACCATCTAAGTTGATTCATAGTGACTGCATATGTTGTG
                        Gaps
                        .,
                       Indels
                       0;
          Pred. No. 1.9e-40;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Fig 13; 168pp; English.
100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DUPO ) DU PONT DE NEMOURS & CO
                                                                                                                                                                                                                                                                                                                 AAT18924 standard; DNA; 4909 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US006689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93US-00077600.
                                                                                                                                                                                                                                                                                                                                                              17-JAN-1997 (first entry)
         al Similarity 100.
243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-036479/05.
                                                                                                                                                                                                                                                         TTC 4312
                                                                                                                                                                                                                                  TTC 243
                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pA126i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9429450-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUN-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                    4070
                                                                                                                                                                                                                                  241
                                                                                                                 4130
                                                                                                                                        121
                                                                                                                                                              4190
                                                                                                                                                                                   181
                                                                                                                                                                                                                                                                                                                                        AAT18924;
                                                                                                                                                                                                                                                                                       Best Loca
Matches
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were designed to mimic the repeating consensus sequence of the natural protein and the pattern of variation among individual repeats. DP-1A analogues are composed of a tandemly repeated 101 amino acid monomer which comprises four repeats which differ from the consensus sequence given in AAW06201, according to the pattern (1)-(5): (1) the poly-alanine sequence varies in length from 0-7 residues; (2) when the entire poly-alanine sequence is deleted, so also is the surrounding sequence encompassing AGRGGLGGCAAAGG; (3) aside from the poly-alanine sequence residues; (4) deletion of GYG is an entire poly-alanine sequence; and (5) a repeat in which the entire poly-alanine sequence; and (5) a repeat in which the entire poly-alanine sequence; a deleted is generally perceded by a repeat containing six alanine residues. The proteins may be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTGAT 2277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITIACAGIATIAIGIAGICIGITITIIIAIGCAAARICIAAITITAAIAIATIGATATITA 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACGTTGGCATTATAAAAAAGCATT 2337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TATCATITITACGTITCTCGTICAGCTTTTTTATACTAAGTIGGCATTATAAAAAGCATT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                           tensile strength and elasticity, suitable for clothing, rope, surr
sutures, biomaterials for implants, plastic reinforcements, films
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4909 BP; 1216 A; 1251 C; 1258 G; 1184 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene; LacZ gene; promoter; vector; pJMF3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 4909;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vector plasmid pJMF3 encoding Lacz-chitobiase fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 243; DB 2; 100.0%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= a
/note= "CAP-cAMP binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function= "Lac promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              function= "Lac promoter'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF30800 standard; DNA; 5641 BP.
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(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 243; Conservative
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Vibrio harveyi.
Bacteriophage lambda.
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Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF4; ds.
                                                                                     Vector plasmid pJMF4 encoding LacZ-chitobiase fusion.
                                                                                                                                                                                                                                                                                                                                                                                     '*tag= d
'note= "Lac repressor binding site'
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "lacZ-chitobiase fusion"
                                                                                                                                                                                                                                                    a
"CAP-cAMP binding
                                                                                                                                                                                                                      location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                         function=
                                                        (first entry)
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1820. .
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                                             (revised)
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                                                                                                                                                                                                                                      .783.
                                                                                                                                                              Vibrio harveyi.
Bacteriophage lambda.
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                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAB20484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                       protein bind
                                          11-SEP-2003
21-JUN-2001
                                                                                                                                                                                                                                      protein bind
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-APR-2001
                                                                                                                                                                                                                                                                                 -35_signal
                                                                                                                                                                                                                                                                                                                             10_signal
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              AAF30801;
                                                                                                                                                                                            Chimeric.
                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
4882
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                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of vector plasmid pJMF3, which includes byage landed attre and the lac promoter with the first 21 amino acids of lack—alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi chitobiase gene (see AAB20484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. A claimed reporter gene construct comprises pJMF3. The invention also comprises expression vectors which express the cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
                                                                                                                                                                                                                                                                                                                           Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transcription within a test sequence; detecting a successful transformation; and for monitoring the activity of a promoter. Chitobiase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   has an advantage over beta-galactósidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4763 TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4823 TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAGGTTGGCATTATAAAAAAGCATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 5641 BP; 1539 A; 1305 C; 1336 G; 1461 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5641;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
 *tag= d
'note= "Lac repressor binding site"
                                                                         /product= "lacz-chitobiase fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 243; DB 4;
100.0%; Pred. No. 1.9e-40;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                        Example 1; Page 32-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      larity 100.0%;
Conservative 0
                                                                                                                                                                02-AUG-2000; 2000WO-US021048
                             1895. .2014
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                                                                                                                                                                                                                         (ELIT-) ELITRA PHARM INC
                                                           partial
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es 243; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4943 TTC 4945
                                                                                                                                                                                                                                                                                                 P-PSDB; AAB20484
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                                                                                                        WO200127322-A2
                                                                                                                                                                                             13-OCT-1999;
                                                                                                                                  19-APR-2001
                                                                                                                                                                                                                                                     Zyskind J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181
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                               CDS
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site"

"Lac promoter"

"Lac promoter'

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Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                 The present sequence is that of vector plasmid pJMF4, which includes phage lambda attP and the lac promoter with the first 21 amino acids of lac2-alpha (from plasmid pUCl9) fused in-frame to the Vibrio harveyi chitobiase gene (see AAB20484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. A claimed reporter gene construct comprises pJMF4. The invention also comprises expression vectors which express the cytoplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transcription within a test sequence, detecting a successful transformation, and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5670 BP; 1567 A; 1302 C; 1356 G; 1445 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 243; DB 4; Length 5670; 100.0%; Pred. No. 1.9e-40;
                                                                                                                                                                                                                              Example 1; Page 34-36; 44pp; English.
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Best Local Similarity
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AAF30801 standard; DNA; 5670 BP.

RESULT 13 AAF30801/c

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121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            claimed reporter gene construct comprises pDYK9. The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. The invention also comprises expression vectors which express the cytoplasmic form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transcription within a test sequence; detecting a successful transformation, and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene system in that it is not necessary to engineer many host
                                                                  TATCATITIACGITICICGTTCAGCTTTTTATACTAAGTTGGCATTATAAAAAGCATT 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence is that of vector plasmid pDYK9, which comprises the Vibrio harveyi chitobiase gene under the control of the Escherichia colidnah promoter in plasmid pACYC184. pDYK9 was used to assess the regulation of the dnah gene using chitobiase as a reporter enzyme. A
                                                                                                                                                      GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT
                       1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise OS field)
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                                                                     Sequence 5826 BP; 1574 A; 1346 C; 1389 G; 1517 T; 0 U; 0 Other
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/product= "dnaA/chitobiase fusion"
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Chimeric.
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The present sequence is that of vector plasmid pDXXII, which comprises the Vibrio harveyi chitobiase gene under the control of the Escherichia coli rpmH-dnah promoter in plasmid pACYC184. The plasmid encodes a dnah-chitobiase fusion protein (see AAB20485). It was used to assess the regulation of the dnah gene using chitobiase as a reporter enzyme. A claimed reporter gene construct comprises pDXXII. The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. The invention also comprises expression cotors which express the cytoplasmic form of chitobiase. Methods are provided for: characterizing a promoter, identifying a regulatory element capable of directing and regulating transcription within a test sequence, detecting a successful transformation; and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity. (Updated on 11-SEP-2003 to standardise of field)
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Sequence 6071 BP; 1638 A; 1400 C; 1451 G; 1582 T; 0 U; 0 Other;

0 Gaps . Query Match 100.0%; Score 243; DB 4; Length 6071; Best Local Similarity 100.0%; Pred. No. 1.9e-40; Matches 243; Conservative 0; Mismatches 0; Indels 0. ð

5133 reretracadereaeranacaretraadracindaritearacideaereaeraretrere 5192 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG

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241 TTC 243

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9, 2004, 18:05:39 Search completed: September Job time: 277.724 secs

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AQ990809 Rfc01638
AQ991303 Rfc02205
AQ990470 Rfc01245
AQ990878 Rfc01715
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GenCore version 5.1.6
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			Bac	steria;	Protec	bact	erië	1; Gammapro	eria; Gammaproteobacteria; E	Enterobacterial	eriales;
	REF	ERENCE		(bases	1 to 7	12)	ŽĮ.	ormandus.			
	Ø	AUTHORS		cench-C	onstant	, К.Н	:	rfi	, Burland, V	., Perna, N	.T.,
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	Σ	MEDLINE		378633						•	
	COM	COMMENT		7/86 act:	ffrench-Constant	נ	10	HR HH			

Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779

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AQ990470 1658 14-AUG-2000 Rfc01245 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG01245, genomic survey
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Enterobacteriaceae; Photorhabdus.

(bases 1 to 769)

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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library"
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88.4%; Score 214.8; DB 28; Length

Best Local Similarity 94.2%; Pred. No. 6.1e-31;

Matches 227; Conservative 0; Mismatches 13; Indels
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/organism="Photorhabdus luminescens"
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                  /db_xref="taxon:29488"
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Photorhabdus luminescens
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firench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn, P.J., Banc,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W4: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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               This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res. Seq primer: M13 Forward Class: shotgun.
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Enterobacteriaceae; Photorhabdus.
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Rfc02205 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02205, genomic survey
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; Pred. No. 2.6e-36;
0; Mismatches 0;
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Department of Biology and Bi
University of Bath
South Building, Bath BA2 7AY
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                  Location/Qualifiers
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Photorhabdus luminescens
Email: bssrfc@bath.ac.uk
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Local Similarity 100.0%;
Les 243; Conservative 0;
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AQ991303.1 GI:9649897
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AQ991303/c
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   Email: bssrfc@bath.ac.uk
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ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,

aborn,P.J., Bowen,D. and Blattner,F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Email: bssrfc@bath.ac.uk
his is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Photorhabdus luminescens genomic clone PLG01715, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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                                                                                                                                                                                                                                                                                                                                                                                               Score 211.4; DB 28; Length 769;
Pred. No. 2.1e-30;
0; Mismatches 13; Indels 1;
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="W14"
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                                                                                      Seq primer: M13 Forward Class: shotgun.
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Best Local Similarity 94.2%;
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BQ157398 472 bp mRNA linear EST 24-APR-2002 NF104D07IR1F1062 Irradiated Medicago truncatula cDNA clone NF104D07IR 5', mRNA sequence.
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Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J.,
Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Medicago truncatula irradiated library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="Genomic DNA from strain W14 was size selected (1-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTGTATTTATATATCA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 703 CAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATGA-ATTTATATCA 645
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          644 TITTTACGTTTCTCGTTCAG-TTTTTTATACTAGTTGCCATTATAAAAAGCATTGCTTA 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             763 TACAGGICACIAAAACCAINIAAGIAGIIGAIICAIAGIGCCNGCAIAIGIIGIGIIIIA 704
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        65
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 28; Length 764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmaymoble.org
Email: gdmaymoble.org
Plate: 104 row: D column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                     /organism="Photorhabdus luminescens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 85.9%; Score 208.8; DB 26
Best Local Similarity 97.5%; Pred. No. 6.5e-30;
Matches 232; Conservative 0; Mismatches 4,
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The Samuel Roberts Noble Foundation
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Medicago truncatula
                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA" /strain="W14"
                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:29488"
/clone="PLG01715"
                                                                                                                                                                                                   Location/Qualifiers
1. .764
                                                                                                                                    Seg primer: M13 Forward Class: shotgun.
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/tissue_rwojacojan
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/clone_lib="Irradiated"
/note="Vector: Lambda Zap; Seedlings were exposed either
/note="Vector: Lambda Zap; Seedlings were exposed either
/note="Vector: Lambda Zap; Seedlings were exposed either
/gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the E. coli strain XLI-Blue MRF'
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A genomic sample sequence of the entomopathogenic bacterium bytornhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                413 TATATTGATATTTATATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTGGCAT 354
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriaceae;
Enterobacteriaceae; Photorhabdus.
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Rfc00126 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00126, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            167 TATAAAAAAGCATTGCTTATCAATTTGCTACGAACAGGTCACTATCAGTCAAAATAA
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Pred. No. 1.3e-27;
                                                                                                           /organism="Medicago truncatula"
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Department of Biology and Biochemistry
University of Bath
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100.0%; Pred. No. 1...
0; Mismatches
                 Seq primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:3880"
                                                                                                                                                                                             clone="NF092E03IR
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Plate: 092
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AQ989566
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COMMENT
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KEYWORDS
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                                                    FEATURES
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                                                                                                                                                          /dev stage="seedling"
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/clone lib="Irradiated"
/note="Vector: Lambda Zap; Seedlings were exposed either
/note="Tector: Lambda Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni: Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-ZAP XR vector using ExAssist
helper phage and the E. coli strain XLI-Blue MRF'
(Stratagene). Excised plasmids were plated using SOLR
cells."
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Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
Unpublished (2001)
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Fig. 580 221 7391
Fax: 580 221 7380
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NF092E03IR1F1023 Irradiated Medicago truncatula cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             167 TATAAAAAGCATTGCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAA 226
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                             organism="Medicago truncatula"
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Insert Length: 473 Std Error: 0.00
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                                                                                                        /clone="NF104D07IR"
/tissue_type="seedlings"
                                                       /mol_type="mRNA"
/db_xref="taxon:3880"
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BQ156404.1 GI:20293463
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BQ156404/c
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COMMENT
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manutaria; kodentia; Sciurogharni; murldae; Murlnae; Mus. 1 (bases 1 to 299)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S., Nikaholi., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
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Gariboldi,M., Gissi,C., Godzik,A., Gough,J., Grimmond,S.,
Kawai,H., Kawaswa,Y., Kedzierski,R.M., King,B.D., Konagaya,A.,
Kawasi,H., Warchioni,L., Morenzie,L., Miki,H., Nagashima,T.,
Numatas,L., Marchioni,L., Morenzie,L., Miki,H., Nagashima,T.,
Numata,K., Okido,T., Pavan,W.J., Pertea,G., Pesole,G.,
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Sandelin,A., Schneider,C., Semple,C.A., Secou,M., Shimada,K.,
Sultana,R., Takenaka,Y., Taylor,M.S., Tasadale,R.D., Tomita,M.,
Verardo,R., Wagner,L., Wahlestedt,C., Wang,Y., Watenabe,Y.,
Wells,C., Wilming,L.G., Wynshaw-Boris,A., Yanagisawa,M., Yang,I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BY115594 BIKEN full-length enriched, 18 days embryo whole body Musmusculus cDNA clone L430040C03 5', mRNA sequence.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
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                                                                                                                                                                                                                                                                                                                                                                                        /note="Genomic DNA from strain W14 was size selected kb) and then cloned into M13 Janus."
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 186.4; DB
Pred. No. 1e-25;
0; Mismatches
                                                                                                                                                                                                              /mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                             /db_xref="taxon:29488"
/clone="PLG01106"
                                                                                                                                Location/Qualifiers
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Mus musculus (house mouse)
                                                                                      Seg primer: M13 Forward
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BY115594.1 GI:26226695
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ilarity 97.7%;
Conservative
                                                                                                                Class: shotgun.
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Best Local Similarity
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BY115594
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1 (bases 1 to 743)

1 (bases 1 to 743)

1 (farench-Constant, R.H., Materfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence 20378633
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                                                                                 This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                80
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Rfc01106 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01106, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13_
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 82679
Fax: (44) 1225 82679
Bani: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the MI3 library. For
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77.1%; Score 187.4; DB 28; Length 751; 95.5%; Pred. No. 6.7e-26; ive 0; Mismatches 8; Indels 2;
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                                                                                                                                                                                                                                                                                     /organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:29488"
/clone="PLG00126"
                                                                                                                                                                                    Seq primer: M13 Forward
Class: shotgun.
    Location/Qualifiers
       Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Photorhabdus luminescens
Photorhabdus luminescens
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Matches 213; Conservative
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574 CAGGICACTATCAGTCAAAATAAAATCATTATTTGATTTC 535
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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                                                                                                                                                                                                                                                                                                                                                         Photorhabdus luminescens
Photorhabdus luminescens
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Class: shotgun.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Fax: 81-45-10-5210

Bmail: genome-res@gsc.riken.go.jp,
URL:http://genome-res@gsc.riken.go.jp/
Aizawa,K., Akimura,T., Arakawa,T., Carninci,P., Fukuda,S.,
Hizozane,T., Imotani,K., Ishi,Y., Itoh,M., Kawai,J., Konno,H.,
Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R.,
Ohno,M., Sakai,K., Sakazune,N., Sasaki,D., Sato,K., Shibata,K.,
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Hayashizaki,Y. Direct Submission
Computational Analysis of Full-Length Mouse cDNAs Compared.with
Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1711 (200)

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CDNA library was prepared and sequenced in Mouse Genome Encyclopedia! Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                      Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 TCTGTCACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATGCAAAATCTAATTTAATATATTGATATTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="18 days embryo"
/clone lib="RIKEN full-length enriched, 18 days embryo
whole body"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             prepare mouse tissues.
Please visit our web site (http://genome.gsc.riken.go.jp) for
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:1090"
/clone="L430040C03"
/tissue_type="whole body"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  76.4%; Score 185.6;
.larity 97.9%; Pred. No. 2e-2
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
                                                                                                                                                                                                                                                                                     Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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Matches 188; Conserv
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ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
AQ990861
RFC01698 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01698, genomic survey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGGICACIATCAGICAAAATAAAAICAITAITIGAITIC 243
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/clone="PLG01698"
/dev_stage="primary phase variant"
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                                                                                                                                                                                                                                                                                                                                                                                       Enterobacteriaceae; Photorhabdus.
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/strain="W14"
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143 634 203 575

694

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Query Match
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Matches
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DEFINITION
                                                       ACCESSION
VERSION
KEYWORDS
SOURCE
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AUTHORS
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PUBMED
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                                                           GSS 14-AUG-2000
                                                                                                                                                                                                                         Encretais, Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.

1 (bases 1 to 746)

1 (bases 1 to 746)

2 (bases 1 to 746)

Butland, V., Perna, N.T.,

Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

20378633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    664 TIGATITIANATCATITITACGTITCTCGTICAGTITITITIATAATTAAGTIGGCATIATA 605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    604 AAAAAGCATTGCTTATCAATTTTGTTGCAACGAACAGGTCACTATCAGTCAAAAAAAT 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         723 ATATGITGIGITTTACAG-ATTATGIAGICIGITTTITTATGCAAAATCTAATTTAATATA 665
                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Fax: (44) 1225 826779
Fax: (52) 122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
                                                       AQ990173 746 bp DNA linear GSS 14-AUG-2
Rfc00898 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00898, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51 ATAIGITGIGITTTACAGTATTATGIAGTCIGITTTTTATGCAAAATCTAATTTAATATA
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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/strain="W14"
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clone="PLG00898"
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Location/Qualifiers
                                                                                                                                                                                            Photorhabdus luminescens
Photorhabdus luminescens
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                                                       LOCUS
                                  AQ990173/c
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AUTHORS
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MEDLINE
PUBMED
COMMENT
                    RESULT 11
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RESULT 12 AQ991774/c

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GSS 14-AUG-2000
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Rfc02368F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02368F, genomic survey
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                                                                                                                                                                                                                                   Photorhabdus luminescens
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Bacteria, Proteobacteria; Gammaproteobacteria; Enterobacteriacea;
1 (bases 1 to 770)
1 (bases 1 to 770)
1 ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
1 ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
2 genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
20378633
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AQ991774 1770 bp DNA linear GSS 14-AUG-20
Rfc02039F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02039F, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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1. 770
/organism="Photorhabdus luminescens"
/mol type="genomic DNA"
/strain="W14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: ffrench-Constant RH
Department of Balology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
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Email: bssrfc@bath.ac.uk
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/clone="PLG02039F"
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AQ991791.1
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AQ991774.1
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ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                                                                      Contact: ffrench-Constant RH
Department of Biology and Biochemistry
Department of Biology and Biochemistry
Department of Biology and Biochemistry
Duith Building, Bath BAZ 7AY, UK
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Fax: (44) 1225 826779
Fax: (44) 1225 826779
Fax: (54) 1225 82677
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Rfc02270 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02270, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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Environ. Microbiol. 66 (8), 3310-3329 (2000)
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/organism="Photorhabdus luminescens"
/mol_type="genomic DNA"
/ktrāin="W14"
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Department of Bilogy and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Enterobacteriaceae; Photorhabdus.
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/clone="PLG01894"
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Photorhabdus luminescens
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Seg primer: M13 Forward
Class: shotgun.
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ffrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
baborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
                                                                                                                firench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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                                Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Photorhabdus luminescens genomic clone PLG01894, genomic survey
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'clone lib="Photorhabdus luminescens strain W14 M13
Library"
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(mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                      Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
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|clone="PLG02368F"
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                                                                                                                                                                                                                                                                                                                                                                                                                            South Building, Bath BA2 7AY,
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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   Photorhabdus luminescens
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AQ991039.1 GI:9649633
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Gaps

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GSS 14-AUG-2000

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Fax: (44) 1225 826779

Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.

Seq primer: M13 Forward
Class: shotgun.

Location/Qualifiers
I. 719

| Corganism="Photorhabdus luminescens"
| About type="genomic DNA" |
| About type="genomic DNA from strain W14 M13 |
| About type="genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
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65.4%; Score 159; DB 28; Length 719;
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Search completed: September 9, 2004, 21:18:23 Job time : 1964.91 secs

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Sequence 173, App
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Sequence 72, Appl
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Sequence 113, App
Sequence 2, Appli
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1: /cgn2_6/ptodata/2/pubpna/USOT_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
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9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_REW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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		1.73 No. US20030226164A1 No. US20030226164A1 No. US20030226164A1 Suttie, Janet Louise Chilton, Mary-Dell Que, Quideng Ge Framond, Anic VENTION: Lambda Inte MICE: 70005USPS MICE: 70005USPS MICE: 2003-03-2 MICE: 2003-03-2 MICHINO NUMBER: US/ MICHIN	Similarity 100.0%; 3, Conservative 0 TCTGTTACAGGTCACTAATA
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Sequence 72, Application US/10161403

Publication No. US20030119104A1

GENERAL INFORMATION

APPLICANT: Perez, Carl

APPLICANT: Derez, Carl

APPLICANT: Lindenbaum, Michael

APPLICANT: Lindenbaum, Michael

APPLICANT: Leung, Josephine

APPLICANT: Fleming, Elena

APPLICANT: Steene, Andre

APPLICANT: Steene, Josephine

APPLICANT: Steener, Joan

TITLE OF INVENTION: CHROMSOME-BASED PLATFORMS

FILE REFERENCE: 24601-420

CURRENT APPLICATION NUMBER: US/10/161,403

CURRENT APPLICATION NUMBER: 60/294,758

PRIOR APPLICATION NUMBER: 60/294,758

PRIOR APPLICATION NUMBER: 60/294,758

PRIOR PILING DATE: 2000-05-30

PRIOR FILING DATE: 2000-03-21

NUMBER: OF SEQ. ID NOS: 129

SOFFWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 100.
Matches 243; Conservative
OTHER INFORMATION: primer
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LENGTH: 282
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Sequence 8, Application US/10627711

Publication No. US20040115812A1

Publication No. US20040115812A1

HIGHER BERNEAL INPORMATION:

TITLE OF INVENTION: SCREENING OF CDNA CLONES

TITLE OF INVENTION: SCREENING OF CDNA CLONES

TITLE OF INVENTION: SCREENING OF CDNA CLONES

CURRENT APPLICATION NUMBER: US/10/627,711

CURRENT FILING DATE: 2002-07-26

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin version 3.2

SEQ ID NO 8

LENGTH: 248
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US-10-695-14
US-10-695-14
Sequence 14, Application US/10310695
Sequence 14. Application WS/10310695
Sequence 14. Application WS/010293A1
GENERAL INFORMATION:
APPLICANT: BENENGE, PETER
TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
FILE REFERENCE: DEBE:019US
CURRENT APPLICATION NUMBER: US/10/310,695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Bacteriophage lambda
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Best Local Similarity 100.0
Matches 243; Conservative
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TTC 243
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LENGTH: 243
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                                 GCTTATCAATTTGTTGCAACGAACAGGTCACTATCAGTCAAAATAAAATCATTATTTGAT 240
                                                        TAICATTITACGTTTCTCGTTCAGCTTTTTTATACTAGGTTGGCATTATAAAAAGCATT 180
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APPLICANT: Lanahan, Anthony
APPLICANT: Lanahan, Anthony
APPLICANT: Gertz, Bernard
APPLICANT: Gertz, Bernard
APPLICANT: Runer, Rohini
APPLICANT: Runer, Rohini
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Chukovski, Bugene
TILLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
TILLE OF INVENTION: IMMEDIATE
FILE REFERENCE: 10496/1004001
CURRENT APPLICATION NUMBER: US/09/244,805
CURRENT PILING DATE: 1998-02-02-05
EARLIER FILING DATE: 1998-02-12
EARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 62
SOFTWARER: FALSKEQ for Windows Version 4.0
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US-09-244-805-57/c
US-09-244-805-57/c
Sequence 57, Application US/09244805
Publication No. US20030203840A1
GENERAL INFORMATION:
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| OTHER INFORMATION: Y = C OF T
| US-09-244-805-57
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Best Local Similarity 100.
Matches 243; Conservative
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NAME/KEY: misc_feature
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ORGANISM: Eukaryote
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RESULT 6 US-09-245-277-57/c

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            SUBJURIES OF SECTION NO. 92,09249.20.//

BUBLICARTION NO. US20030211984A1

GENERAL INFORMATION:

APPLICANT: Worley, Paul F.

APPLICANT: Lanahan, Anthony

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: 19199-02-05

FILE REFERENCE: 1999-02-05

FRICA PLICATION NUMBER: 06/074,518

PRIOR FILING DATE: 1999-02-05

PRIOR FILING DATE: 1998-02-12

PRIOR FILING DATE: 1998-02-06

NUMBER OF SEQ ID NOS: 63

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 57

LENGTH: 1763

TYPE: DNA

ORGANISM: EUKARYOLE

NAME/FORV. Min. ELANARYOLE

FRAURE: NAME/FORV. Min. ELANARYOLE
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APPLICANT: Lanahan, Anthony
APPLICANT: Goetz, Bernard
APPLICANT: Heimisch, Holger
APPLICANT: Kuner, Rohini
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Zhucovski, Eugene
TITLE OF INVENTION: IMMEDIATE BARLY GENES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
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100.0%; Score 243; DB 11;
Best Local Similarity 100.0%; Pred. No. 1.9e-40;
Matches 243; Conservative 0; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/792,481
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/99/244,805
PRIOR FILING DATE: 1999-02-05
PRIOR APPLICATION NUMBER: 60/074,518
Sequence 57, Application US/09245277
Publication No. US20030211984A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
CCATION: (1)...(1763)
OTHER INFORMATION: y = C or T
OTHER INFORMATION: n = A,T,C or G
US-09-245-277-57
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Publication No. US20040152658A1
GENERAL INFORMATION:
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RESULT 10
US-10-270-176-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Perkins, Edward
APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Blena
APPLICANT: Steart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOWE-BASED PLATFORMS
TITLE OF INVENTION: CHROMOSOWE-BASED PLATFORMS
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: PASLSEQ for Windows Version 4.0
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PRIOR FILING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: 60/074,135
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 57
LENGTH: 1763
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                                                                                                                                                                   NAME/KEY: misc_feature; LOCATION: (1)...(1763)
OTHER INFORMATION: y = C or T
COTHER INFORMATION: n = A,T,C or G
US-10-792-481-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                ORGANISM: Bukaryote
FEATURE:
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US-10-161-403-113
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                                                                                                                         TYPE: DNA
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Publication No. US20040110293A1
GENERAL INFORMATION:
APPLICANT: BETER
APPLICANT: ENENUEL, BARBARA
ITITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
FILE REPERRENCE: DEBE:019US
CURRENT APPLICATION UNDER: US/10/310,695
CURRENT SILVING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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98.8%; Pred. No. 1e-39;
tive 0; Mismatches 3;
Pred. No. 2.6e-40;
; Mismatches 0;
          Best Local Similarity 100.0%; P. Matches 243; Conservative 0;
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ORGANISM: Artificial Sequence
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Best Local Similarity 98.8
Matches 240; Conservative
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US-10-310-695-2
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LENGTH: 3695
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                                            APPLICANT: Haldimann, Andreas
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
FILE REPERENCE: 290.001401011
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/328,642
PRIOR APPLICATION NUMBER: 60/378,059
PRIOR APPLICATION NUMBER: 60/375,059
PRIOR APPLICATION NUMBER: 60/375,059
PRIOR APPLICATION NUMBER: 60/375,059
PRIOR APPLICATION NUMBER: 60/375,059
SPRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PALENTIN VERSION 3.0
SEQ ID NO 8
LENGTH: 2959
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Publication No. US20040033608A1
GENERAL INFORMATION:
APPLICANT: Wanner, Barry
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
FILE REFERENCE: 290.00140101
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2001-0-10
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
Sequence 8, Application US/10270176
Publication No. US20040033608A1
GENERAL INFORMATION:
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; OTHER INFORMATION: CRIM plasmid
US-10-270-176-8
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Best Local Similarity 99.2
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: artificial
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             Length 3663;
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95.1%; Score 231; DB 13; Length 3695;
Best Local Similarity 99.2%; Pred. No. 7.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2
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US-10-270-176-13
Sequence 13, Application US/10270176
Sequence 13, Application US/10270176
SUBJICATION NO. US20040033608A1
GENERAL INFORMATION:
APPLICANT: Wanner, Barry
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
FILE REPERENCE: 290.00146010
CURRENT APPLICATION NUMBER: 05/10/270,176
CURRENT FILING DATE: 2002-10-10
PRIOR FILING DATE: 2001-10-10
PRIOR PLICATION NUMBER: 60/375,059
PRIOR PLICATION NUMBER: 60/375,059
PRIOR PLICATION NUMBER: 60/375,059
                                                               Indels
        Score 231; DB 13;
Pred. No. 7.1e-38;
0; Mismatches 0;
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        95.1%;
99.2%;
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SOFTWARE: PatentIn version 3.0
Query Match
Best Local Similarity 99.2°
Matches 243; Conservative
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; OTHER INFORMATION: CRIM plasmid US-10-270-176-41
                                                                                                      Matches 243; Conservative
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                                                                    Query Match
Best Local Similarity
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APPLICANT: Haldimann, Andreas
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
FILE REFERENCE: 290.00140101
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT APPLICATION NUMBER: 60/328,642
PRIOR FILING DATE: 2002-10-10
PRIOR PILING DATE: 2001-10-10
PRIOR PLING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
SOCTWARE: Patentin version 3.0
SEQ ID NO 41
LENGTH: 5646
                                                                                                                            APPLICANT: Wanner, Barry
APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
FILE REPRENCE: 290, 00140101
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: 60/338,642
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-10-424
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PALENTIN Version 3.0
SEQ ID NO 20
LENGTH: 4782
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ilarity 99.2%; Pred. No. 7.7e-38;
Conservative 0; Mismatches 0;
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                                                                          ; Sequence 20, Application US/10270176; Publication No. US20040033608A1; GENERAL INFORMATION:
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Matches 243; Conserv
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US-10-270-176-41
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95.1%; Score 211; DB 13; Length 5706;
Best Local Similarity 99.2%; Pred. No. 8.1e-38;
Matches 243; Conservative 0; Mismatches 0; Indels 2;
    Length 5646;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Manner, Barry
APPLICANT: Haldimann, Andreas
APPLICANT: Haldimann, Andreas
APPLICANT: Haldimann, Andreas
FILE COF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
FILE REFERENCE: 200.00140101
CURRENT APPLICATION NUMBER: 60/120,642
CURRENT FILING DATE: 2002-10-10
FRIOR FILING DATE: 2001-10-10
FRIOR FILING DATE: 2001-10-10
FRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
SOGTWARE: Patentin Version 3.0
SEQ ID NO 40
LENGTH: 5706
                                               Indels
Score 231; DB 13;
Pred. No. 8.1e-38;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: CRIM plasmid
       95.1%;
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239 ATTTC 243 |||||| 4208 ATTTC 4212

Qy Dp

Search completed: September 10, 2004, 00:14:07 Job time: 307.981 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model	Run on: September 9, 2004, 15:48:15; Search time 704.078 Seconds (without alignments) 6279.120 Million cell updates/sec	Title: US-10-082-772B-3 Perfect score: 102 Sequence: 1 ctgctttttatactaagtttaaaaatcattatttgatttc 102	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	Searched: 3470272 segs, 21671516995 residues	Total number of hits satisfying chosen parameters: 6940544	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	Database : GenEmbl:*  1:
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	14 Seque Human d	325746 Homo	Seque	AR063063 Sequence 193548 Sequence 69	AR370418 Sequence	AX449167 Sequence	X52304 Chlamydomon	AR309120 Sequence	AR372694 Sequence RD007602 Nematoda	AR080463 Sequence	M57625 Mouse prote A71437 Semience 7	AR207455 Sequence	BD069511 Improved A71440 Semience 10	AR207458 Sequence	BDU69514 IMPIOVED AB069968 Oryza sat	AJ428542 Zea mays	AP002533 Escherich	M91470 Trypanosoma	E05439 Oligonucleo	113139 Sequence 18	AX092113 Sequence	M23841 Bacteriopha	AATOLOOO SEGUENCE D85521 Macaca fasc	BD225932 Immediate	AY048723 CRIM plas	4 7	116	8733	2 G		1000 TEAM-10 TEAM	oz wil tz tut thoms		eria; Enterobacteriales;		eukaryotic cells
SUMMARIES	AX092114 HUMDTN02	HSA325746 AF121976		ARU63U63 I93548	AR370418 AX430197	AX449167	CRPERAS A91914	AR309120	AR372694 BD007602	AR080463	MUSPROT6A A71437	AR207455	BD069511 A71440	AR207458	AB069968	ZMA428542	AP002553	TREGPSSB	E05439	113139	AX092113	LAMINTATT AX101000	MACHSS	BD225932	΄ Ω	AF178449	2.5	5	4	ALIGNMENTS	102 by	WO0116345.	57	eria, Gammaproteobacteria; Rscherichia		recombination in 3 08-MAR-2001;
% Query Match Length DB	0.00	.0 1090 9 .0 1421 10	00.0 2408 6	00.0 2408 6	00.0 2408 6	00.00 3049 6	00.0 3111 8	000.0 3484 6	00.0 3484 6 00.0 3484 6	000.0 3757 6	00.0 3757 10 00.0 5349 6	00.0 5349 6	00.0 5611 6	00.0 5611 6	0.00 6803 8	0.00	00.0 297816 1	0 2934 3	4 201 6	4 201 6	4 243 6	4 361 7	4 1668 9	4 1763 6 4 2758 3	4 2959 12	4 3485 12	4 3663 12	4 3695 12	4 4190 12		AX092114	Sequence 3 from Patent	92114.1 GI:134443	Escherichia coli Escherichia coli Bacteria; Proteobacteria; Enterchacteriaceae. Reche	age, P.	ra
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Mammalia, Butheria, Primates, Catarrhin; Hominidae, Homo.

1 (bases 1 to 1090)

Kutsenko, A.S., Gizatullin, R.Z., Al-Amin, A.N., Wang, F., Kvasha, S.M.,
Podowski, R.M., Matushkin, Y.G., Gyanchandani, A., Muravenko, O.V.,
Levitsky, V.G., Kolchanov, N.A., Protopopov, A.I., Kashuba, V.I.,
Kisselev, I.I., Wasserman, W., Wahlestedt, C. and Zabarovsky, E.R.
Not I flanking sequences: a tool for gene discovery and verification
of the human genome
Nucleic Acids Res. 30 (14), 3163-3170 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi; Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 442 to 1421)
Malnic,B., Hirono, Sato,T. and Buck,L.B.
Combinatorial receptor codes for odors
                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (16-MAY-2001) Microbiology and Tumorbiology Centre,
Karolinska Institute, Theorells vag, 3, Box 280, Stockholm 171 77,
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Direct Submission
Submitted (07-DEC-1999) Neurobiology, Harvard Medical School, 220
Longwood Avenue, Boston, MA 02115, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
Homo sapiens genomic sequence surrounding NotI site, clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1090;
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Mus musculus odorant receptor S19 gene, complete cds.
AF121976
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Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
Direct Submission
Submitted (20-JAN-1999) Neurobiology, Harvard
Longwood Avenue, Boston, MA 02115, USA
3 (bases 1 to 1421)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="NB1-850S"
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Mus musculus
                                                           GI:15870140
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Zabarovsky, E.R.
                                                                                                Homo sapiens (human)
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                                                                                                                Homo sapiens
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,

(Dases 1 to 979)

Sadoulet-Puccio, H.M., Feener, C.A., Schaid, D.J., Thibodeau, S.N.,

Michels, V.V. and Kunkel, L.M.

The genomic organization of human dystrobrevin

Neurogenetics 1 (1), 37-42 (1997)
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Sadoulet-Puccio,H.M., Feener,C.A. and Kunkel,L.M.
Direct Submission
Submitted (09-JAN-1997) Genetics, HHMI, 320 Longwood Avenue,
Boston, MA 02115, USA
1. Ocation/Qualifiers
1. 979
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Pred. No. 1.6e-14;
0; Mismatches 0; Indels ()
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                                                                              /mol_type="unassigned DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
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                                                            /organism="Escherichia
                         Location/Qualifiers
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U84530
                                                                                                                                                         100.0%;
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450. .530
/gene="DTN"
/number=2
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Best Local Similarity 100.0
Matches 102; Conservative
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Matches 102; Conservative
       Peter (DE)
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Sequence 69 from patent US 5844072.
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Sequence 69 from patent US 6300470.
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/organism="unknown"
/mol_type="unassigned
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AR063063.1 GI:5990754
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YTELEDQHVWTAIPFCSMYILALVGNGTILYIITDRALHEPMYLFLCLLSITDLVLC
STTLEPMLATFWLRSHVISYHGCLTQMFFVHATBGAVLLAMAFDRXVAICRPHY
TSILMANVIGKIGLACVTRGLLFVFPVILIERLPFCGHHIIPHTVCEHMGIAKLACA
SIKRNTIYGLTVALSVTGMDVULTATSYILLIQAVLRLPSKDAQFRAFSTCGAHICU
LVFYIPAFFSFFTHRFGHHVPPQVHIILANLYLLVPFVINPLNYGINTKQIRLRLDF
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Sequence update by submitter
On Dec 7, 1999 this sequence version replaced gi:4680261.
Location/Qualifiers
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                                                                                                                                                     291. .1310
/note="G-protein-coupled receptor"
                                                                                                                         <291. .>1310
/product="odorant receptor S19"
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/protein_id="AAD27596.2"
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Selsted, M.E. and Ouellette, A.J.
Antibiotic cryptdin peptides and met
Patent: US 5840498-A 69 24-NOV-1998;
Location/Qualifiers
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<291. .>1310
                                                                                                                                                                                                                                'db_xref="GI:6532001"
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DEFINITION ACCESSION

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RESULT 6 AR063063

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Unclassified.
Lobases 1 to 2408)
Selsted, M.B. and Ouellette, A.J.
Antiblotic oryptidn peptides and methods of their use
Patent: US 5844072-A 69 01-DEC-1998;
Location/Qualifiers
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Selsted, M.E. and Ouellette, A.J.
Antibiotic cryptdin peptides and methods of their use
Patent: US 5731149-A 69 24-MAR-1998;
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     1 (bases 1 to 2408)
Selsted, M.B. and Ouellette, A.J.
Antibiotic cryptdin peptides and methods of their use
Patent: US 6300470-A 69 09-OCT-2001;
Location/Qualifiers
1..2408
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100.0%; Pred. No. 9e-15;
tive 0; Mismatches 0; Indels
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100.0%; Score 102; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.4e-15;
Matches 102; Conservative 0; Mismatches 0;
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| Organism="Beta vulgaris"
|/mol_type="unassigned DNA"
| db_xref="taxon:161934"
| 1. .2998
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Sequence 4 from Patent W00240687.
AX449167.1 GI:21697968
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                                                                                            /organism="unknown"
/mol_type="genomic DNA"
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de Hostos, E.L.
Direct Submission
Submitsed (11-APR-1990) De Hostos E.L., Max-Planck-Institude for
Submistry, Am Klopferspitz 18A, 8033 Martinsried, FRG
The sequence is a composite of a cDNA (for CDS region) and genomic.
See <XI6179> for intron between bases 717-718.
See <XI6180> for bases 616-3104.
Location/Qualifiers
1.3111
1.3111
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophyllales; Amaranthaceae; Beta.
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I baese 481 to 3111)
de Hostos, B.L., Schilling, J. and Grossman, A.R. Structure and expression of the gene encoding the periplasmic Structure and expression of the gene encoding the periplasmic Mol. Gen. Genet. 218 (2), 229-239 (1989)
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100.0%; Score 102; DB 6; Length 3
Best Local Similarity 100.0%; Pred. No. 9e-15;
Matches 102; Conservative 0; Mismatches 0; Indels
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X52304
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/mol_type="mRNA"
/strain="CW15."
/db_xref="taxon:3055"
/clone lib="Lambda gt11 (cDNA) and BMB 481. 566
                                                                                                                                                                                                              location/Qualifiers
1.3049
/organism="Beta vulgaris"
/mol type="unassigned DNA"
/db_xxef="taxon:161934"
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/note="transcription start
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/note="inverted repeat A'"
616. .2556
                                                                                                                                          Tissue specific promoters
Patent: WO 0240687-A 4 23-MAY-2002;
KWS Saat AG (DE)
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                                                                                                                    Hehl, R., Kloos, D. and Stahl, D.J.
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2877. .2883
2928. .3049
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Query Match
Best Local Similarity 100.0%;
Matches 102; Conservative 0,
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AR372694
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                                                                                                                           / LTAINS LAKY IRYPONARANGUANASVAHAADTKKRNEVVI FUDDQDAIQNST
HPHYNDS LAKY IRYPGVELSQY FVTTPVCCPSRTNLCAASSPTTPTSPACCLEPTVAGP
SRAMASTSPTCRCGSRTRAITPTTMASSLWTTPSATTSRCRGLGRYRCPYTPTY
NYTLORNGATPNI YPGRYSTDVI INDKGVAQI KSAVAAGKPFYAQI SPI APHTSTDI NYTLORNGATPNI YPARPHYDLI SEGSQOBPLRGGRERQARLDPRAAGPBE
QPHLPGGDL.PPAPPHWQLFSDANL.PGGSQOBPLRGGRERQARLDPRAAGPBE
QPHLPGGDL.PPAPPHWGLI EQVVKTLDEAGVLDNIYI I YSADNGYHVGAHRFGA
GKTTGYBEDLRVPFLLRGPGI KASKSNKPQNSKVGLHVDFAPTI LGLAGASHLLGDKG
                                                                                                                                                                                                                                                           LDGTPLGLYANDDGTLPSDYPREEDHQQFQSEFWGGMSDETLQNLRSQPNUTWKVVN
TYDESSKQGMKLIAQCTNRRELYDLRKDPGRELYNIYDKAKFAVRSRLEGLLAVLAVCK
GESCSNPWKILHPDGTVKYFTQALNSKYDRIYNATRPFTYKRCLPYLDWDNEDSQFKT
QIRGAMPAAQVGHHLLTAASERAIATRRRAQAAVSAELADGPAVFQAKVEEKSVPVP
QDILKADVEKWFAFNNAEYYLA"
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'note="unnamed protein product; protein precursor (AA -21
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Arabidopsis thaliana
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
1 closes I to 3484)
1 (bases I to 3484)
1 (bases I to 3484)
1 (bases I to 3484)
1 REMATODE-INDUCIBLE REGULATORY DNA SEQUENCES
Patent: WO 9822599-A I 28-MAY-1998;
EEF FREDERIQUE MARIANNE D (NL); OHL STEPHAN ANDREAS (NL)
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100.0%; Pred. No. 9e-15;
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/note≈"signal peptide (AA -21 to -1)"
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/product="mature protein (AA 1-625)"
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                                                                                                                xref="SWISS-PROT:P14217"
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                                                          /proteIn_id="CAA36545.1"
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Sequence 1 from Patent W09822599.
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1 (bases 1 to 3484)
2 (bases 2 to 3484)
3.A., Sijmons, P.C., Klein-Van der Lee, F.M., Goddijn, O. and
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Funaba,Y., Koike,J., Tanahashi,M., Okazaki,S. and Ito,M.
Remedies for intramedullary diseases
Patent: US 6555529-A 1 29-APR-2003;
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Nematode-inducible regulatory DNA sequences
Patent: US 6395963-A 1 28-MAY-2002;
Location/Qualifiers
; Score 102; DB 6;
; Pred. No. 8.8e-15;
0; Mismatches 0;
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Sequence 1 from patent US 6395963.
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/wol_type="genomic DNA"
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

CE 1 (bases I to 3484)

Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

CE 2 (bases I to 3484)

Nomatoda-induced regulatory DNA sequence

AL Nomatoda-induced regulatory DNA sequence

AL Nomatoda-induced regulatory DNA sequence

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                                                                    1. .3484
Corganism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
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Location/Qualifiers
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JP 2001503992-A/1.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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Search completed: September 9, 2004, 19:34:31 Job time : 706.078 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

9, 2004, 13:30:05; Search time 116.156 Seconds (without alignments) 3730.479 Million cell updates/sec September Run on:

US-10-082-772B-3

1 ctgcttttttatactaagtt.......taaaatcattatttgatttc 102 Perfect score: Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

6747726 Potal number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

N\_Geneseq\_29Jan04:\* 1: geneseqn1980s:\* geneseqn1990s:\* geneseqn1980s:\* Database :

geneseqn2003as:\* geneseqn2003bs:\* genesedn2001as:\* geneseqn2001bs:\* geneseqn2003cs:\* geneseqn2004s:\* geneseqn2000s:\* geneseqn2002s:\* 8: 9: 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Aaf61419 E. coli a		Abn81284 Beet prom		Aav44332 Murine mM	Aav42708 Mouse mas	Aav23239 T-DNA of	Aav23242 Plasmid p			Acc85316 Recombina	Acc44676 Murine rD			Abq80306 Lambda fr		Aaz30709 Rat neuro	Acc44716 Plasmid p	Abt16615 Artificia	Aat18924 Plasmid p	Aaf30800 Vector pl	Vector	
SUMMARIES	<b>:</b>	ID	AAF61419	AAT30737	ABN81284	AAV34987	AAV44332	AAV42708	AAV23239	AAV23242	AAQ50319	AAF61418	ACC85316	ACC44676	ABT16636	AAF79770	ABQ80306	ACC83020	AAZ30709	ACC44716	ABT16615	AAT18924	AAF30800	AAF30801	AAF30798
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٥	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4	98.4
	6	Score	102	102	102	102	102	102	102	102	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4	100.4
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Aaf30799 Vector pl	Aaq45682 Sequencin	Aaf61421 E. coli a	Aal62713 Escherich	Aac55386 Recombina	Acc59569 Nucleic a	Aac55422 Entry vec	Aac55437 Entry vec	Abz58764 Entry vec			Aac55434 Entry vec	Entry	Aac55446 Entry vec	Aac55443 Entry vec	Aac55449 Entry vec	Aac55440 Entry vec	Aac55452 Entry vec	Adc06860 Plasmid p	Adc06864 Plasmid p	Abk88866 Topoisome	Ade83789 Plasmid p
AAF30799	AAQ45682	AAF61421	AAL62713	AAC55386	ACC59569	AAC55422	AAC55437	ABZ58764	AAC55425	AAC55431	AAC55434	AAC55428	AAC55446	AAC55443	AAC55449	AAC55440	AAC55452	ADC06860	ADC06864	ABK88866	ADE83789
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98.4	98.4	96.9	96.5	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	92.0	95.0	92.0	92.0	92.0	90.4	90.4	90.4	90.4
100.4	100.4	98.8	98.4	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	93.8	92.2	92.2	92.2	92.2
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## ALIGNMENTS

AAF61419 standard; DNA; 102 05-JUN-2001 AAF61419; RESULT 1 AAF61419 

BP

(first entry)

E. coli attL DNA fragment,

Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attl; ds.

Escherichia coli.

DE19941186-A1.

01-MAR-2001.

99DE-01041186. 30-AUG-1999;

99DE-01041186. 30-AUG-1999;

(DROE/) DROEGE

Droege P;

WPI; 2001-246016/26.

Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites.

Claim 3; Page 14; 24pp; German.

This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in sometic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences

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Sequence 2408 BP; 640 A; 531 C; 557 G; 680 T; 0 U; 0 Other;
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                                                                     1 CIGCITITITATACTAAGTIGGCATTATAAAAAGCATTGCTTATCAATTTGTIGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cryptdin peptide(s) - which have antimicrobial activity, in the detection and treatment of inflammatory pathologies.
                                                                                                                                                                                                                                                                                                                                           /codon start= 1174. .1176 /note= "exon 1 codes for the 5' untranslated region and
                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= c
/note= "exon 2 codes for cryptdin-2 and 3' untranslated
                                                          1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                       Gaps
                                                                                                                                                                                                                                                    Cryptdin 2; antibiotic; antimicrobial; defensin; inflammation; antiinflammatoxy; inflammatory bowel disease; pancreatitis; cancer;
                                      0;
                   Length 102;
                                      Indels
                                                                                                             61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                 61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
Sequence 102 BP; 35 A; 16 C; 13 G; 38 T; 0 U; 0 Other;
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                 Score 102; DB 4;
Pred. No. 4.5e-19;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 31; Page 64~65; 103pp; English.
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                                                                                                                                                                      AAT30737 standard; DNA; 2408 BP
                   100.0%;
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P-PSDB; AAR98787, AAR98792.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouellette AJ;
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                                                                                                                                                                                                               entry)
                                       102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                              1931.
                                                                                                                                                                                                                                                              antiinflammatory; in tumour; ileitis; ds.
                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                Rat cryptdin 2 gene.
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9616075-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       used partic.
                                                                                                                                                                                                              20-0CT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selsted ME,
                                                                                                                                                                                                                                                                                             Rattus sp
                                                                                                                                                                                         AAT30737;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SHRI-)
                                                                                                                                                                                                                                                                                                                                                                            intron
                                        Matches
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                                                                                                                                                               408 crecrititraractaagriggcarraraaaaagcarrecriarcaarrigriggaag 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New tissue-specific promoters from Beta vulgaris, useful e.g. for altering carbohydrate metabolism, express transgenes selectively in roots
                                                                                                                09
                                                                                                                CTGCTTTTTTATACTAGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beet; promoter; carbohydrate metabolism; invertase inhibitor;
fructosyl transferase; levan sucrase; nitrogen transporter protein;
pathogen resistance; plant; transgenic; ds.
                                                     0;
Length 2408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3049 BP; 783 A; 699 C; 876 G; 691 T; 0 U; 0 Other;
                                                        Indels
                                                                                                                                                                                                                                61 AACAGGTCACTATCAGTCAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                        468 AACAGGTCACTATCAGTCAAATAAAATCATTATTTGATTTC
100.0%; Score 102; DB 2; 100.0%; Pred. No. 6.5e-19;
                                                        0
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Beet promoter polynucleotide SEQ ID NO 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 30-31; 57pp; German.
        ABN81284 standard; DNA; 3049
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2877. .2883
/*tag= c
2928. .3049
/*tag= b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2000EP-00124989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .2998
                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-437465/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (KWSS-) KWS SAAT AG
                          Local Similarity
hes 102; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kloos D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or aerial parts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATA_signal
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AAV4433
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                                                                                       2398 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 2457
                               o;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Arabidopsis thaliana DNA promoter - useful for, e.g. generating plant reduced susceptibility to plant parasitic nematodes.
                                                             09
                                                          CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
                               Gaps
                                                                                                                                                                                                                                                                                                                                                             Promoter; nematode feeding site; root knot nematode; cyst nematode;
Meloidogyne incognita; Heterodera schachtii; Globodera pallida;
transgenic plant; pest resistance; crop protection; ds.
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 Length 3049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goddijn OJM, Klap J, Sijmons PC;
                               Indels
                                                                                                                                      2458 AACAGGICACIATCAGICAAAAIAAAAICAITATIIGAIIIC 2499
                                                                                                                                                                                                                                                                                                                               Arabidopsis nematode feeding site-preferential promoter.
                                                                                                                    61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
Query Match 100.0%; Score 102; DB 6; Best Local Similarity 100.0%; Pred. No. 6.7e-19; Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start= 3482. .3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 22-24; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana; ecotype C24.
                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                          AAV34987 standard; DNA; 3484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97WO-EP006472,
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                                                                                                                                                                                                                                                                                     (revised)
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Van Der Lee FM,
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                                                                                                                                                                                                                                                                                     17-OCT-2003
28-SEP-1998
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a plant cell having incorporated into its genome the chimeric DNA of (2); (6) a root system of a plant consisting of the cells of (5); (7) a plant consisting of the cells of (5); (7) a plant consisting of the cells of (5); (8); a plant, especially a potato plant; (8) a plant grafted onto the root system of (6); (9) a part of a plant; selected from seeds, flowers, tubers, roots, leaves, fruits, pollen and wood, obtained from the plant of (7) or (8), and (10) a crop consisting of the plants of (7) or (8). The DNA fragment can be used to identify subtragments capable of promoting transcription of an associated DNA sequence in a plant. It can also be used for making hybrid regulatory DNA sequences. The chimeric DNA sequence of (2) can be used for transforming plants (all claimed). The DNA sequence can be used to reduce the susceptibility of a plant to parasitic nematodes. (Updated on 17-OCT-2003 to standardise OS field)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CIGCITITITATACTAAGTIGGCATTATAAAAAAGCATIGCITATCAATTIGITGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MCP-6 zymogen; mouse; mast cell protease 6; mMCP-7; tryptase-7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              blood clot; anticoagulant; myocardial infarction; reocclusion; thromboembolism; cerebral embolism; thrombosis; therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 102; DB 2; Length 3484; 100.0%; Pred. No. 6.8e-19; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                Sequence 3484 BP; 1143 A; 583 C; 625 G; 1133 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
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'note= "contains introns"
1803. .1872
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2012. .2177
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2861. .2933
/*tag= i
/number= 4
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1873. .2011
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*tag= e
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/number= 3
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Best Local Similarity 100.0
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exon

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6). The invention provides sequences shown in AAW63160 to AAW6169 that are inhibitors of mMCP-6. These peptides which are tryptase-6 complex inhibitors, can be used for treating a mast cell-mediated inflammatory disorder. The inhibitors can be used to treat inflammatory disorders including asthma, allergic rhinitis, uriticaria and anticedema, eczematous dematitis, (atopic dermatitis), hyperproliferative skin disease, anaphylaxis, peptic ulcers, inflammatory bowel disorder, hyperresponsiveness and inflammatory skin conditions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 374 CIGCITITITATACTAAGTIGGCATTATAAAAAGCATIGCTIATCAAITIGTIGCAACG 433
                                                                                                                                                                                                                       Tryptase-6 complex inhibitory peptides - used to treat mast cell-mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barstar; barnase inhibitor; fertility restoration; male-sterile line;
                                                                                                                                                                                                                                                                                                                                This represents the cDNA sequence of the mouse mast cell protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "region coding for phosphinothricin acetyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              containing 3' untranslated end -- DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3757 BP; 802 A; 1014 C; 1003 G; 938 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    434 AACAGGICACTATCAGICAAAATAAAATCATTATITGATTTC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 102; DB 2;
100.0%; Pred. No. 6.8e-19;
live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agrobacterium T-DNA gene
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/note= "right boarder"
complement(98. .331)
                                                                                                                                                                                                                                                                                     Disclosure; Page 42-43; 69pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                            inflammatory disorders e.g. asthma
                                                                                                (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (1. .25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAV23239 standard; DNA; 5349 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lote= "region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 102; Conservative 0
                 98WO-US001865
                                                          97US-0037090P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= bar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid pTTS24; T-DNA; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *tag=
                                                                                                                                           Stevens RL, Huang C;
                                                                                                                                                                                  WPI; 1998-437390/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     T-DNA of pTTS24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1998
                     30-JAN-1998;
                                                          05-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAV23239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAV23239/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This nucleotide sequence includes a coding region for mouse mast cell procease 6 (mMCP-6, see AAW64242). The invention provides: compositions comprising an isolated tryptase-7 (such as mMCP-7, see AAW64233); a method for treating a blood clot by administering a nucleic acid molecule that codes for a tryptase-7, or an expression product; a nucleic acid encoding a serine procease (SP); and a method of producing a mature SP. Tryptase-7 polypeptides can be used for treating disorders mediated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             undesirable thrombus clot formation such as myocardial infarction and reocclusion following angioplasty of blood clots associated with pulmonary thromboembolism, deep vein thrombosis, cerebral embolism, renal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   374 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCCATTGCTTATCAATTTGTTGCAACG 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mast cell protease; MCP; mouse; inhibitor; peptide substrate; asthma; tryptase-6 protein; inflammatory disorder; allergic rhinitis; urticaria; artioedema; eczematous dermatitis; atopic dermatitis; anaphylaxis; hyperproliferative skin diseas; peptic ulcer; hyperresponsiveness; inflammatory skin condition; ss.
                                                                                                                                                                                                                                                                                                                                                                                          New compositions containing tryptase-7, e.g. mouse mast cell protease-7 are used to treat clot formation in e.g. myocardial infarction, reocclusion following angioplasty or pulmonary thrombo-embolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGCTTTTTTATACTAGGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 3757;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3757 BP; 802 A; 1014 C; 1003 G; 938 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse mast cell protease (mMCP-6) nucleic acid sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           434 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Score 102; DB 2;
; Pred. No. 6.8e-19;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vein and peripheral arterial thrombosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 68-69; 92pp; English.
                                                                                                                                                                                                                                              (BGHM ) BRIGHAM & WOMENS HOSPITAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV42708 standard; cDNA; 3757 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                 97WO-US021620
                                                                                                                                                                                                        96US-0032354P
    2934. .3098
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                           /number=
                         /*tag=
                                                                                                                                                                                                                                                                                                                                WPI; 1998-333308/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW64242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9833812-A1
                                                                                                                                                                   25-NOV-1997;
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                                                                                 WO9824886-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-AUG-1998
                                                                                                                          11-JUN-1998
                                                                                                                                                                                                                                                                                            Stevens RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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AAV42708 RESULT

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Gaps

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/label= 3' nos
/note= "region containing 3' untranslated end of nopaline
synthase gene of Agrobacterium T-DA"
complement(318. .869)
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                                                                                                                                                                                                                                                                                                                                                                                 /*tag= f
//label= 3'_chs
/note= "region containing 3' untranslated end of chalcone
synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence was used in the preparation of an improved Bacillus amyloliquefactens barstar, i.e. barnase inhibitor, which can be used to restore fertility to male-sterile lines. The DNA sequence encoding the improved barstar, leads to increased barstar production in tapetum cells, due to improved translation, and possibly protein stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGCTTTTTTATACTAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA encoding an improved barstar protein - used to restore fertility in male-sterile plant lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                             note= "promoter of TA29 gene of Nicotiana tabacum"
285. .2560
                                                                                                                                                  /note= "region coding for phosphinothricin acetyl transferase"
                                                                                                                                                                                                                                  note= "35S promoter of Cauliflower Mosaic Virus"
740. .2284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5611 BP; 1389 A; 1342 C; 1353 G; 1527 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 102; DB 2; Length 5 Best Local Similarity 100.0%; Pred. No. 7.2e-19; Matches 102; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AACAGGTCACTATCAGTCAAAATTAAAATCATTATTTGATTTC 3099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                product= "improved barstar"
                                                                                                                                                                                complement (870. .1702)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 45-48; 54pp; English.
     Location/Qualifiers
complement (39. .317)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ĭ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PLBZ ) PLANT GENETIC SYSTEMS
                                                                                                                                                                                                                                                                  *tag= d
label= PTA29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97WO-EP004739.
                                                                                                                 /*tag≈ b
/label= bar
                                                                                                                                                                                                     *tag= c
label= P35S
                                                                                                                                                                                                                                                                                                                                                              2561. .2892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAQ50319 standard; DNA; 201
                                     '*tag= a
'label= 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams M;
                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-193630/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9810081-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Michiels F,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3140
                                                                                                                                                                                                                                                 promoter
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                                                                                                                                                                                    promoter
     Key
3'UTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ50319
ID AAQ5
XX
AC AAQ5
                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                  CDS
                                                                                                                                                                                                                                                                                                                                                                CDS
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     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4885 CIGCITITITATACTAAGITGGCALTATAAAAAGCALTGCTTATCAALTIGLTGCAACG 4826
                                                                                                                                                              '*tag≈ g
|label= 3' chs
|note= "region containing 3' untranslated end of chalcone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amyloliquefacions barstar, i.e. barnase inhibitor, which can be used to restore fettility to male-seraile lines. The DNA sequence encoding the improved barstar, leads to increased barstar production in tapetum cells, due to improved translation, and possibly protein stability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence was used in the preparation of an improved Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA encoding an improved barstar protein - used to restore fertility in male-sterile plant lines.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CTGCTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barstar; barnase inhibitor; fertility restoration; male-sterile line; plasmid pLH48; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
           note= "35S promoter of Cauliflower Mosaic Virus"
281. .3969
                                                                                 rice (WO9213956)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5349 BP; 1339 A; 1233 C; 1290 G; 1487 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4825 AACAGGTCACTATCAGTCAAAAAAAATCATTATTTGATTTC 4784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 102; DB 2;
100.0%; Pred. No. 7.1e-19;
tive 0; Mismatches 0;
                                                                                 뜡
                                                              label= PE1
note= "promoter of E1 gene
1970. .4245
                                                                                                                            product= "improved_barstar
                                                                                                                                                                                                                                               '*tag= h
'note= "T-DNA left border"
                                                                                                                                                                                                                              complement (5325. .5349)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; Page 41-43; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           (PLBZ ) PLANT GENETIC SYSTEMS NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthase gene"
label= P35S
                                                                                                                                                                                                                                                                                                                                                            97WO-EP004739
                                                                                                                                              246. .4577
                                                                                                .4245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                 *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-193630/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 102; Conserv
                                                                                                                                                                                                                              misc_feature
                                                                                                                                                                                                                                                                                                                                                           01-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                             03-SEP-1996;
                                                                                                                                                                                                                                                                                               WO9810081-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Michiels F,
                                                                                                                                                                                                                                                                                                                              12-MAR-1998
                                  promoter
                                                                                                                                              CDS
                                                                                               CDS
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27-APR-1994

17-SEP-1993

Synthetic.

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DNA in a enkaryotic cell, comprising introducing two DNA sequences (I, into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences
                                                                           Sequence-specific recombination of DNA in eukaryotes, useful particulariy for somatic cell gene therapy, uses an integrase to effect recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Site-specific integration of DNA into plastid DNA, useful for making transgenic plants used e.g. as food, by recombinase-mediated insertion.
                                                                                                                                                                                                       This invention describes a novel sequence-specific recombination (SSR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a method for the site-specific integration of a DNA sequence into the plastid DNA of a plant or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vegetable plastid transformation; transgenic; recognition sequence; plant; site-specific integration; nutrition; seed production; chemical production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 100.4; DB 4; Length 243;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinase lambda integrase attP DNA recognition sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 243
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 35; 164pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SUNG-) SUNGENE GMBH & CO KGAA.
                                                                                                                                                                Claim 2; Page 13; 24pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20-DEC-2001; 2001DE-01063159.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.0%;
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-2002; 2002WO-EP014303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACC85316 standard; DNA; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                    WPI; 2001-246016/26.
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                                                                                                                           between att sites.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2003054201-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biesgen C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142
Droege P;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACC85316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACC8531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequences given in AAQ50309-26 are probes which were used on a chip for capturing a number of target polynucleotides. A group of these probes may be attached on cells which form part of a single chip. The oligonucleotides to be detected are labelled and are complementary to the set of capture probes used. The detection chip may be used to detect a number of different polynucleotides concurrently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                     Chip for capturing polynucleotide - has several different complementary probes fixed on cells at different sites on single tip.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attP; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGCTTTTTTTATACTAGGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 100.4; DB 2; Length 201; Pred. No. 1.3e-18; 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AACAGGICACIAICAGICAAAAIAAAAICAIIAIIIGAIIIIC 144
                                                                                                     Probe; chip; cell; detection; label; capture probe; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 201 BP; 58 A; 38 C; 27 G; 78 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage lambda attP DNA fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 8; 10pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAF61418 standard; DNA; 243 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99DE-01041186
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                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                     (HITA ) HITACHI LTD
                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1993-330600/42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                Detection probe 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ᆄ
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                                                                                                                                                                                       JP05236997-A
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                                                                                                                                                                                                                                                                          28-FEB-1992;
                                                                                                                                                                                                                                                                                                                 28-FEB-1992;
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05-JUN-2001

AAF61418;

RESULT 10 AAF61418

61 103

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Query Match

01-MAR-2001

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Gaps

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one or several att sites, where an att site is heterologus to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described. (1) a platform artificial chromosome expression system (Aces) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (1) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform artificial artificial chromosome, preferably an ACes. (II) is useful for producing a
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                    206
derived cells. Transgenic plants in which a DNA sequence has been integrated, also their cell cultures, organs, tissues etc. are useful in human or animal nutrition, to produce seeds, and to produce pharmaceuticals or fine chemicals, e.g. erzymes, vitamins, amino acids, flavourings and aromatizing agents, dyes, autibodies and vaccines. The present sequence is a recognition sequence shown in the exemplification
                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chromosome-based platform, artificial chromosome, eukaryotic chromosome, att site; integrase, recombinase, ACes, gene therapy, transgenic animal, platform artificial chromosome expression system; gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a eukaryotic chromosome (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                               1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                                                                                                      147 CAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAAGG
                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                   DB 8; Length 248;
                                                                                                                                                                                                                                                                                                                                                            61 AACAGGICACIAICAGICAAAAIAAAAICAIIAIIIGAIIIC 102
                                                                                                                                                                                                                                                                                                                                                                                  207 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 248
                                                                                                                                                            Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;
                                                                                                                                                                                                                        Pred. No. 1.4e-18;
                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                 98.4%; Score 100.4; 99.0%; Pred. No. 1.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 2; Page 207; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine rDNA PCR primer SEQ ID NO:72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACC44676 standard; DNA; 282 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2002; 2002WO-US017452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2001; 2001US-0294758P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2002US-0366891P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-MAY-2003 (first entry)
                                                                                                                                                                                                                                        Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perez C,
Shellard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-140461/13.
                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200297059-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perkins E,
Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  interest
                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACC44676
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                                                                            cell, preferably a stem cell or an embryo. (II) comprises a heterologous mucleic acid that encodes a therapeutic product which is useful for making a library of Aces comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                   156 CAGCITITITATACTAAGTIGGCATTATAAAAAGCATIGCTTATCAATTIGTIGCAACG 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, tRNA, tRNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and
                                                                                                                                                                                                                                                                                                                             1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
transgenic animal (e.g. a fish, insect, reptile, amphibian, arachmid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinfection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant artificial chromosome, PAC, transgenic plant, vaccine,
blood factor, herbicide, stress, agronomical, nutrient quality,
bacterial artificial chromosome, BAC, yeast artificial chromosome, YAC,
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                            DB 7; Length 282;
                                                                                                                                                                                                                                            Score 100.4; DB 7; Length Pred. No. 1.4e-18; 0; Mismatches 1; Indels
                                                                                                                                                                                                      Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                              61 AACAGGICACIAICAGICAAAAIAAAAICAIIAIIIGAIIIC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                   AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Artificial plant chromosome related oligo SEQ ID No 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 263-264; 269pp; English.
                                                                                                                                                               exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHROMOS MOLECULAR SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2001; 2001US-0294687P. 04-JUN-2001; 2001US-0296329P.
                                                                                                                                                                                                                                              98.4%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABT16636 standard; DNA; 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perez C, Fabijanski SF,
                                                                                                                                                                                                                                                                                         Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGRISOMA INC
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                                                                                                                                                                                                                                            Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHRO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AGRI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABT16636
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280 CAGCTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 339

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61

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340 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 381

Primer; PCR; amplify; lambda phage; printer material; insertion; deletion; single nucleotide polymorphism; sequencing; diagnosis;

Lambda fragment in plasmid DNA.

(first entry)

27-JUN-2003

ABQ80306;

ABQ80306 standard; DNA; 1469

RESULT 15 ABQ80306

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                                                                                                                                                                                                                                                                                                     156 CAGCTITITITATACTAGGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 215
                                                                                                                                                                                                                                                                         09
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biopharmaceutical proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (RAC). This polymucleotide sequence represents an oligo relating to the method for producing plant artificial chromosomes of the invention
                                                                                                                                                                                                                                                                        1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Attachment P region; attP; recombination; marker gene removal; ds.
                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                             Length 282;
                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                       216 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 257
                                                                                                                                                                          Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                   61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                           DB 7;
                                                                                                                                                                                                        Score 100.4; DB 7
Pred. No. 1.4e-18;
                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage lambda attachment P region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Fig 3D; 25pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99GB-00021937.
                                                                                                                                                                                                           98.4%;
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                                                                                                                                                                                                      Query Match
Best Local Similarity 99.0
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage lambda
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                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
AAF79770
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24-SEP-2002; 2002WO-JP009766 25-SEP-2001; 2001JP-00291249

WO2003027991-A1.

Synthetic.

03-APR-2003.

(DNAF-) DNAFORM KK (RIKE ) RIKEN KK. WPI; 2003-354676/33.

Hayashizaki Y;

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The sequences given in ABQ80304-05 are primers which were used to amplify DNA for use in the material of the invention. The primers amplify a 1377 DNA for use in the material of the invention. The print of a plasmid. The amplified is sequence (ABQ80306) was attached to the printer material of the invention of sequence (ABQ80306) was attached to the printer material of the invention which comprises at least one support having at least one oligomer and/or comprises at least one support having at least one oligomer and/or synthesising DNA where the product of amplification and/or ligation is constantation of nucleotide insertion/deletion, single nucleotide confidence of determination of nucleotide insertion/deletion, or SNP analysis.

Colymportide or protein expression. The printed material is useful in cresearch applications, or for providing scientists with oligomer and/or polymers from the printed materials easily and immediately. From the colymport of activities and/or polymer can be obtained immediately and directly, without need to make a request for it. The oligomers and/or polymers can be delivered and stored easily with reduced the facilities while eliminating the need to use special equipment or facilities may be anywork of a mick, efficient and the material is a mick, efficient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Printed material useful as a delivery and storage system for oligomer and/or polymer, comprises a support having an oligomer and/or polymer applied on it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      printed material is a quick, efficient and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Page 31-32; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   facilities. Thus, the printed mater
inexpensive sample delivery system
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0; Score 100.4; DB 7; Length 1469; Pred. No. 1.7e-18; 0; Mismatches 1; Indels 0; Query Match 98.4%; Best Local Similarity 99.0%; Matches 101; Conservative (

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Gaps

÷ 0

Indels

98.4%; Score 100.4; DB 5; Length 610; ilarity 99.0%; Pred. No. 1.5e-18; Conservative 0; Mismatches 1: Thiale n

Best Local Similarity Matches 101; Conserv

Query Match

Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;

by flanking the transgene with a bacteriophage lambda attachment P (attP) region and inducing homologous recombination between attP regions so that the transgene is removed. This is useful in the production of transgenic

plants with less risk of inter-species transmission of marker genes, which often encode proteins associated with, for example, herbicide an antibiotic resistance. The present sequence is the attp coding region

The present invention describes a method of removing a transgene marker

ó;

Gaps

 QY
 1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
 60

 Db
 949 CAGCTTTTTTATACTAAGTTGGCATTATAAAAAAAGCATTGCTTATCAATTTGTTGCAACG
 1008

 QY
 61 AACAGGTCACTATCAGTCAAAAAAAAACATTATTTGATTTC
 102

 Db
 1009 AACAGGTCACCTATCAGTCAAAATCATTATTTGATTC
 1050

Search completed: September 9, 2004, 18:05:40 Job time: 117.156 secs

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92122
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Sequence 18, Appl
Sequence 18, Appl
Sequence 78, Appl
Sequence 4, Appli
Sequence 1, Appli
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Sequence 50, Appl
Sequence 66, Appl
Sequence 24, Appl
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69, Appl
1, Appli
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Sequence 3, Appli
Sequence 3, Appli
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                                                                                  9, 2004, 17:33:11; Search time 22.4903 Seconds (without alignments) 2516.866 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 69, P
Sequence 69, P
Sequence 69, P
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'/ Ggn2_ 6/ptodata/2/ina/5A_COMB.seq:*
'/ Ggn2_ 6/ptodata/2/ina/5B_COMB.seq:*
'/ Ggn2_ 6/ptodata/2/ina/6A_COMB.seq:*
'/ Ggn2_ 6/ptodata/2/ina/6B_COMB.seq:*
'/ Ggn2_ 6/ptodata/2/ina/PCTUS_COMB.seq:*
'/ Cgn2_ 6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-486-013-69
US-08-482-279-69
US-08-342-268-69
US-09-301-968-69
US-09-301-968-69
US-09-308-090-1
US-09-016-366A-13
US-09-016-366A-13
US-09-016-101-7
US-09-068-101-7
US-09-068-101-7
US-09-068-101-10
US-08-101-544-18
US-08-101-544-18
US-08-101-53EA-18
US-08-56-978B-78
US-09-53-978B-78
US-09-53-978B-78
US-09-53-978B-78
US-09-53-702B-50
US-09-453-702B-66
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US-09-453-702B-66
US-09-453-702B-66
US-09-453-702B-66
US-09-453-702B-66
US-09-453-702B-68
US-09-453-702B-68
US-08-98-11DE-269
US-08-98-11DE-269
US-08-98-11DE-269
US-08-98-11DE-269
US-08-98-711E-269
US-08-98-711E-269
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                                                                                                                                                                                                                                                 682709 seqs, 277475446 residues
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Maximum Match 100%
Listing first 45 summaries
                                                       using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seg length: 2000000000
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102
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Match Length DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Selsted, Michael E. APPLICANT: Obellette, Andre J. TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods TITLE OF INVENTION: of Their Use NUMBER OF SEQUENCES: 70 ADDRESSED: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 1; Length 2408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3: Campbell and Flores
4370 La Jolla Village Drive, Suite 700
                                                                                          VS-08-308-8738-1

VS-08-318-8738-1

US-08-314-0016-2801

US-09-134-0016-2801

US-09-621-976-14383

US-09-821-976-14383

US-08-142-368A-25

US-08-142-368A-25

US-08-97-727-25

US-08-937-2300-25

US-09-583-850-25

US-09-583-850-25

US-09-583-850-25

US-09-583-850-25

US-09-583-850-25

US-09-40-026-25

US-09-40-026-25
                          US-09-854-799-21
PCT-US91-08525-21
                                                                          PCT-US93-04384-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Cambell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P.UC 1206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 530
FILING DATE:
APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-NAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 69, Application US/08486013; Patent No. 5731149; GENERAL INFORMATION:
                     4365
4365
4365
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602
654
580073
                                                                                                                                                                                                      STRANDEDNESS: single
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CITY: San Diego
STATE: California
COUNTRY: USA
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408 CIGCITITITATACTAAGITGGCATTATAAAAAGCATTGCTTATCAATTIGITGCAACG 467
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                          RESULT 3
US-08-342-268-69
US-08-342-268-69
; Sequence 69. Application US/08342268
; Patent No. 5844072
; GENERAL INFORMATION:
; APPLICANT: Salsted, Michael E.
; APPLICANT: Ouellette, Andred E.
; TITLE OF INVENTION: of Their Use
; TITLE OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS: 70
; CORRESPONDENCE ADDRESS: 70
; CORRESPONDENCE ADDRESS: 70
; STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 69, Application US/09015968
; Patent No. 6057425
; GENERAL INFORMATION:
    APPLICANT: Selsted, Michael E.
    APPLICANT: Ouellette, Andre J.
    TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
    TITLE OF INVENTION: of Their Use
    NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: Campbell and Flores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 2408;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE PATENTIN STILL SOFTWARE WITH SEPARATION SOFTWARE PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,268
FILING DATE: US/08/342,268
FILING DATE: US/08/342,268
FILING DATE: US/08/342,268
FILING DATE: US/07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION NUMBER: US 07/989,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 102; DB 2;
Best Local Similarity 100.0%; Pred. No. 4.1e-20;
Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFRENCE/DOCKET NUMBER: P-UC 1206
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
INPORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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: California
RY: USA
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US-09-015-968-69
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                                                                                                                                                                                                                                                                                                                                                                                         STATE:
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                                                                                                                                  408 CIGCITITITATACTAAGITGGCATTATAAAAAGCATTGCTTATCAATTIGTTGCAACG 467
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                                                                                  1 CIGCITITITATACIAAGIIGGCAITAIAAAAAAGCAIIGCIIAICAAIIIIGIIGCAACG 60
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                                  Gaps
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Sequence 69, Application US/08482279
Patent No. 5840498
GENERAL INFORMATION:
APPLICANT: Selsted, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 102; DB 2; Length 2408; 100.0%; Pred. No. 4.1e-20; Live 0; Mismatches 0; Indels 0
                                  Indels
                                                                                                                                                                                    61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                    468 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AACAGGTCACTATCAGTCAAAAAAAATCATTATTTTGATTTC 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PILLING DATE: US/08/482,279
FILING DATE:
                                     ;
0
       Pred. No. 4.1e-20;
                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/342,268

FILING DATE: 18-NOV-1994

APPLICATION NUMBER: US 07/930,649

FILING DATE: 14-AGG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/889,020

FILING DATE: 26-MAY-1992

ATTORNEY/AGENT IRFORMATION:

NAME: Campbell, Cathryn A.

REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-UC 1206

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001

TELEPHONE: (619) 535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.08;
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Matches 102; Conservative
                               Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 4370 La Ju
CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
          Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    US-08-482-279-69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-482-279-69
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09-397-386-69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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APPLICANT: Selsted, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSED: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 102; DB 3; Length 2408; 100.0%; Pred. No. 4.1e-20; cive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 AACAGGICACTAICAGICAAAAIAAAAICAITAITIIGAITIC 102
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4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8449
INFORMATION FOR SEQ ID NO: 69: SEQUENCE CHARACTERISTICS:
LENGTH. 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY AGENT INFORMATION:
NAME: Cambhall Cathyrin A
                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 69, Application US/09397386
Patent No. 6300470
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.(
Matches 102; Conservative
                     CITY: San Diego
STATE: California
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                                                                   USA
                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
US-09-015-968-69
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                                                                   COUNTRY:
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408 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 467
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Sequence 1, Application US/09308090

Patent No. 6395963

GENERAL INFORMATION:
APPLICANT: Oll, Stephan
APPLICANT: Van Der Lee, Frederique
APPLICANT: Sijmons, Peter
APPLICANT: Sijmons, Peter
TITLE OF INVENTION Nematode-Inducible Regulatory DNA Sequences
FILE REFERENCE: NG 57680
CURRENT APPLICATION NUMBER: US/09/308,090
CURRENT APPLICATION NUMBER: PCT/EP97/06472
ERALIER FILING DATE: 1999-05-14
ERALIER FILING DATE: 1996-11-18
ERALIER FILING DATE: 1996-11-18
ERALIER FILING DATE: 1996-11-18
ERALIER PLING DATE: 1996-11-18
ERALIER NEW SEQ ID NOS: 10
SOFTWARE: PATENTIN Ver. 2.0
ERQ ID NO 1
ELMOSTH: 3484
ELMOSTH: NAMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             468 AACAGGTCACTATCAGTCAAATAAAATCATTATTTGATTTC 509
                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                        FILING DATE:

APPLICATION NUMBER: US 08/482,279
FILING DATE: US 07-UN-1995
PRIOR APPLICATION NUMBER: US 08/342,268
FILING DATE: US 00/-1994
APPLICATION NUMBER: US 08/342,268
FILING DATE: US -00/-1994
PRIOR APPLICATION NUMBER: US 07/930,649
FILING DATE: US -00/-1992
PRIOR APPLICATION NUMBER: US 07/889,020
FILING DATE: US 07/889,020
FILING DATE: US 07/889,020
FILING DATE: CS -MAY-1992
ATTORNEY/ACSNT INFORMATION:
REGISTRATION NUMBER: P-UC 3003
FILECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION SEG 1D NO: 69:
SEQUENCE CHARACTERISTICS:
TENGENCE CHARACTERISTICS:
TENGENCE CHARACTERISTICS:
                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,386
                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.
Matches 102; Conservative
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                                                                                                                                               FILING DATE:
CLASSIFICATION:
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374 CIGCITITITIATACTAAGITGCCATTATAAAAAGCATIGCTTATCAATTIGTIGCAACG 433
                                                                                                                                                                                                                                             420 CIGCITITITIATACTAAGTIGGCATTATAAAAAAGCATIGCTIATCAATTIGIIGCAAGGA79
                                                                                                                                                                                                       1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG
                                                                                                                                                             Gaps
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0
                                                                                                                Length 3484;
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                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                              61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                            480 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 521
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                                                                                                              100.0%; Score 102; DB 4;
100.0%; Pred. No. 4.3e-20;
vative 0; Mismatches 0;
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100.0%; Pred. No. 4.3e-20;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 8
US-09-016-366A-13
Squence 13, Application US/09016366A
Sequence 13, Papalication US/0901636A
Patent No. 5955431
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
APPLICANT: Huang, Chifu
TITLE OF INVENTION: MAST CELL PROTEASE PEPTIDE
TITLE OF INVENTION: NHIBBITORS
LOCATION: 3481..3484
OTHER INFORMATION: /codon_start= 3482
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONTINENT AND COMPACTATION OF SOFTWARE: FASTSEQ for Windows Version 2.0 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/016,366A
FILING DATE: January 30, 1998
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/037,090
FILING DATE: 05-FEB-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 65
CORRESSONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7093
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U.S.A.
ZIP: 02210-2211
COMPUTER READABLE FORM:
MEDLUM TYPE: DISKette
COMPUTER: IBM COMPAIDLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 3757 base pairs
                                                                                                                  Query Match 100.
Best Local Similarity 100.
Matches 102; Conservative
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Matches 102; Conserv
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STREET: boc
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: li
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-016-366A-13
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US-09-380-090A-1
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                                                                                                                                                                                                                                   420 CHGCTTTTTTATACTAAGTTGGCATTATAAAAAAAGCATTGCTTATCAATTTGTTGCAACG 479
                                                                                                                                                                                         9
                                                                                                                                            Gaps
                                                                                                                                            0:
                                                                                                                                                                                         1 CIGCITITITATACIAAGIIGGCAITAIAAAAAAGCAIIGCITAICAAITIGI
                                                                                                  Length 3484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA SEQUENCES
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/380,090A
FILING DATE: 17-May-1999
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION: AUNKNOWN>
                                                                                                                                                                                                                                                                             61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTTGATTTC 102
                                                                                                                                                                                                                                                                                                                          480 AACAGGICACTAICAGICAAAIAAAICAITAITIIGAITIC 521
                                                                                                100.0%; Score 102; DB 4;
100.0%; Pred. No. 4.3e-20;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO PCT/EP97/06472
FILING DATE: 18-NOV-1997
APPLICATION NUMBER: EP 96203213.2
FILING DATE: 18-NOV-1996
ATTORNEY/AGRNT INFORMATION:
NAME: Superko, Colleen
REGISTRATION NUMBER: 39,850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OHL, Stephan Andreas
SIJMONS, Peter Christiaan
KLEIN-VAN DER LEE, Frederique
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: SYN-010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Arabidopsis thaliana STRAIN: C24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Hale and Dorr LLP
STREET: 60 State Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 526-6000
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09380090A
Patent No. 655529
GENERAL INFORMATION:
APPLICANT: OHL, Stephan Andre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (617) 526-5000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3484 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: United States
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GODDIJN, Oscar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Massachusetts
                                                                                             Query Match
Best Local Similarity 100.0
Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marianne
    ; NAME/KEY: CDS
; LOCATION: (3482)..(3484)
US-09-308-090-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE
                                                                                                                                                                                                                                                                                                                                                                                            RESULT 7
US-09-380-090A-1
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EARLIER FILING DATE: 1996-09-03
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US-09-068-101-10/c
                                                                                         5349
                                                                   SEQ ID NO 7
                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          374 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 100.0%; Score 102; DB 2; Length 3757; Best Local Similarity 100.0%; Pred. No. 4.3e-20; Matches 102; Conservative 0; Mismatches 0; Indels 0
                                         434 AACAGGICACTATCAGICAAATAAATCATTATTIGATTIC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 AACAGGICACTATCAGTCAAAATAAATCATTATTTGATTTC 475
                                                                                                                                                   Sequence 19, Application US/08978404B
Patent No. 5968782
GENERAL INFORMATION:
APPLICANT: Stevens, Richard L.
TITLE OF INVENTION: MAST CELL PROTEASE THAT CLEAVES
TITLE OF INVENTION: FIBRINOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURENT APPLICATION DATA:
APPLICATION NUMBER: US/08/978,404B
FILING DATE: 25-NOV-97
                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESSES: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: PLANT GENETIC SYSTEMS N.V.
TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2121-139P
CURRENT APPLICATION NUMBER: US/09/068,101
CURRENT FILING DATE: 1998-08-26
EARLIER APPLICATION NUMBER: EP 96202446.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: B0801/7090
TELECOMMUNICATION:
TELEPHONE: 617-720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 25-NOV-97
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/032,354
FILING DATE: 04-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7, Application US/09068101
Patent No. 6372960
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 3757 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 02210-2211
                                                                                                          RESULT 9
US-08-978-404B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
TOPOLOGY:
US-08-978-404B-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-068-101-7/c
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4885 CIGCITITITATACTAAGTIGGCAITATAAAAAAGCAITGCITATCAAITIGTIGCAACG 4826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: (4246)..(4577)
OTHER INFORMATION: label = 3'chs, "region containing 3' untranslated
OTHER INFORMATION: end of chalcone synthase gene"
                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "T-DNA of pTTS243"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: Complement((884)..(2258))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus"
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: Complement((332)..(883))
OTHER INFORMATION: label = bar, "region coding for phosphinthricin
OTHER INFORMATION: acetyl transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (2281)..(3969)

OTHER INFORMATION: label = PE1, "promoter of E1 gene of rice (WO OTHER INFORMATION: 92/13956)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((98)..(331))
OTHER INFORMATION: label = 3'97, "region containing 3'
OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (3970)..(4245)
OTHER INFORMATION: label = synb*; "improved barstar
                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: Complement((1)..(25))
OTHER INFORWATION: label = RB, "T-DNA right border"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_feature
; ICCATION: Complement((5325)..(5349))
; OTHER INFORMATION: label = LB, "T-DNA left border"
US-09-068-101-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
100.0%; Score 102; DB 4;
Best Local Similarity 100.0%; Pred. No. 4.6e-20;
Matches 102; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 10, Application US/09068101; Patent No. 6372960; CENERAL INFORMATION:
; APPLICANT: PLANT GREETIC SYSTEMS N.V.; TITLE OF INVENTION: Improved Barstar Gene; FILE REFERENCE: 2121-139P; CURRENT APPLICATION NUMBER: US/09/068,101; CURRENT FILING DATE: 1998-08-26; EARLIER APPLICATION NUMBER: EP 96202446.9
                                                                                                                              TYPE: DNA ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 10 SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature
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FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520..
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-828-0300
TELEPHONE: 202-828-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98.4%;
                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 99.0°
Matches 101; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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US-08-021-667A-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: D
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTGCTTTTTTATACTAGTTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Okano, Kazunori
APPLICANT: Okano, Kazunori
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3' untranslated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene of Nicotiana
                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: Complement((39)..(317))
OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated
OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium
OTHER INFORMATION: T-DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: Complement((870)..(1702))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "plasmid pLH48"
                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: Complement((318)..(869))
OTHER INFORMATION: label = bar, "region coding for phosphinothricin
OTHER INFORMATION: acetyl transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 102; DB 4; Length 5611; 100.0%; Pred. No. 4.6e-20; rive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3140 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 3099
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KRY: misc_feature
LOCATION: (2285)..(2560)
OTHER INFORMATION: label = synb*, "improved barstar DNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PEATURE:
NAME/KEY: misc feature
LOCATION: (2561)..(2892)
OTHER INFORMATION: label = 3'chs, "region containing
OTHER INFORMATION: end of chalcone synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (1740)..(2284)
OTHER INFORMATION: label = PTA29, "promoter of TA29
OTHER INFORMATION: tabacum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
US-08-021-667A-18
; Sequence 18, Application US/08021667A
; Patent No. 5434049
EARLIER FILING DATE: 1996-09-03
                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 10
LENGTH: 5611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Virus"
                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE: NAME/KEY: misc_feature
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STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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ZIP: 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-068-101-10
                                                                                                                                                                FEATURE:
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43 CAGCTITITIATACTAAGTIGGCATTATAAAAAGCATIGCTTATCAATTIGTIGCAACG 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 18, Application US/08410544
; Sequence 18, Application US/08410544
; Patent No. 5607646
; GENERAL INFORMATION:
; APPLICANT: Okano, Kazunori
; APPLICANT: Application POLYNUCLEOTIDE CAPTURING TIP AND
; TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
; TITLE OF INVENTION: METHOD USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AACAGGICACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTG 144
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
AURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,667A
FILING DATE: 19930224
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: Suite 600, 1919 Pensylvania Ave., NW
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CR-9389-A
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; Sequence 78, Application US/08556378B
Patent No. 6268169
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBJI
TITLE OF INVENTION: SPIDER SILK AN
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/AGENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRALION NUMBER: 33,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 33,692
RELECOMMUNICATION INFORMATION:
TELEPHONE: 302-8112
TELEFAX: 302-773-016/
                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4909 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                      Best Local Similarity 99.0
Matches 101; Conservative
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Best Local Similarity 99.0
Matches 101; Conservative
          TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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CITY: WILMINTON
STATE: DELAWARE
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CLASSIFICATION:
                                                                                                           õ
                                                                                                         ; ANTI-SENSE:
US-08-728-785A-18
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Patent No. 5817506
GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                               Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                   1 CTGCTTTTTTATACTAGGTTGGCATTATAAAAAGCATTGCTTATCAATTT
                                                                                                                                                                                                                                                                                                                                                                                    Indels
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I: Suite 1800, 1300 No. 5817506th Seventeenth St.
Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               103 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 144
                                                                                                                                                                                                                                                                                                                                         Score 100.4; DB 1;
Pred. No. 8.1e-20;
0; Mismatches 1;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATUR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,785A
FILING DATE: 10-OCT-1996
CLASSIFICATION: 435
                      520.31930X00
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APPLICATION NUMBER: 08/410,544
FILING DATE: 21-MAR-1995
PRIOR APPLICATION DATA:
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FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
                REFERENCE/DOCKET NUMBER: 52
TELECOMUNICIONIND INPORMATION:
TELEPHONE: 202-828-0300
TELEFAX: 202-828-0380
  20,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
                                                                                                                      18:
                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
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SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
                                                                                                                                                     LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                    TELER: 202-828-0380
TELEX: 248545
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 99.0°
Matches 101; Conservative
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                             US-08-410-544-18
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43 CAGCTITITATACTAAGTIGGGATTATAAAAAGCATTGCTTATCAATTIGTIGCAACG 102
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                                                                                           1 CIGCITITITATACTAAGTIGGCATTAIAAAAAAGCATIGCTIATCAAITIGTIGCAACG
                                                       Gaps
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     Length 201;
                                                     1; Indels
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                                                                                                                                                                                                                                            103 AACAGGICACTATCAGICAAAATAAAATCATTATTIGATTIC 144
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98.4%; Score 100.4; DB 1;
99.0%; Pred. No. 8.1e-20;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.4%; Score 100.4; DB 3; 99.0%; Pred. No. 1.3e-19; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19898
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOVEL RECOMBINANTLY SPIDER SILK ANALOGS
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61 PACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
2315 AACAGGTCACTATCAGTCAAAAAAATAAAATCATTATTTGATTTC 2274 Qy Dp

Search completed: September 9, 2004, 21:21:19 Job time : 23.4903 secs

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5; Search time 184.482 Seconds (without alignments) 3730.479 Million cell updates/sec
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                     9, 2004, 13:30:05
                                                                                           OM nucleic - nucleic search, using sw model
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1 totgttacaggtcactaata.....agcttttttatactaacttg 162 US-10-082-772B-4 Title: Perfect score: Sequence:

IDENTITY\_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

6747726 Total number of hits satisfying chosen parameters:

3373863 seqs, 2124099041 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003cs:\* geneseqn2004s:\* geneseqn2001as:\* geneseqn2001bs:\* geneseqn2003bs:\* N\_Geneseq\_29Jan04:\* 1:\_geneseqn1980s:\* genesegn2003as: geneseqn1990s:\* geneseqn2002s:\* geneseqn1980s:\* geneseqn2000s:\* •• Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

	Description			Acc85316 Recombina	Acc44676 Murine rD	Abt16636 Artificia		Abq80306 Lambda fr					Plasmi	Aaf30800 Vector pl	Aaf30801 Vector pl	Aaf30798 Vector pl	Aaf30799 Vector pl		Aaf61421 E. coli a	Abq82142 Acceptor	Abq82142 Acceptor	Abq82141 Acceptor	Abq82141 Acceptor	Abq82143 Acceptor
	ΩÏ	AAF61420	AAF61418	ACC85316	ACC44676	ABT16636	AAF79770	ABQ80306	ACC83020	AAZ30709	, ACC44716	ABT16615	AAT18924	1 AAF30800	1 AAF30801	1 AAF30798	4 AAF30799	2 AAQ45682	4 AAF61421	5 ABQ82142	5 ABQ82142	5 ABQ82141	5 ABQ82141	5 ABQ82143
	DB	4	4	80	7	7	2	7	7	7	7	7	2	4	4	4	4	~	4	9	9	9	φ	φ.
	Query Match Length	162	243	248	282	282	610	1469	1.469	1763	4346	4346	4909	5641	5670	5826	6071	7652	243	17458	17458	17476	17476	17681
*	Query Match	100.0	99.0	0.66	0.66	0.66	0.66	99.0	99.0	99.0	99.0	99.0	99.0	99.0	0.66	0.66	99.0	99.0	98.0	94.1	94.1	94.1	94.1	94.1
	Score	162	160.4	160.4	160.4	160.4	160.4	160.4	160.4	160.4	160.4	160.4	160.4	160.4	160.4	160.4	160.4	160.4	158.8	152.4	152.4	152.4	152.4	152.4
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ABQ82143	AAC55522	AAC55523	AAC55521	ABZ58767	ADA50329	AAC55525	AAC55632	ABZ58766	ABQ82130	ABQ82130	AAC55382	ACC59568	AAC55524	AAC55522	AAC55523	ABZ58768	AAC55521	ABZ58767	ABZ58769	ABZ58770	ADA50329	
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94.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.1	93.0	93.0	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92.1	92 1	1
152.4	150.8	150.8	150.8	150.8	150.8	150.8	150.8	150.8	150.8	150.8	150.6	150.6	149.2	149.2	149.2	149.2	149.2	149.2	149.2	149.2	149 2	117.1
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## ALIGNMENTS

RESULT 1

Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attR; ds. BP. AAF61420 standard; DNA; 162 (first entry) E. coli attR DNA fragment. Escherichia coli. DE19941186-A1. 05-JUN-2001 AAF61420; AAF61420 

99DE-01041186. 99DE-01041186. 30-AUG-1999; 30-AUG-1999; 01-MAR-2001.

WPI; 2001-246016/26. 다. (DROE/) DROEGE Droege P;

Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites.

Claim 3; Page 14; 24pp; German.

This invention describes a novel sequence-specific recombination (SSR) of DNA in a enkaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (1) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) vector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy in humans and animals, but can be applied more generally for gene transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences

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Unidentified
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                                                                                                                               RESULT 3
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                                                                                                                            TITTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATGTATTTA 120
                                                                                                                 TITIATGCAAAATCTAATTTAATATATTGATATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel sequence-specific recombination (SSR) of DNA in a eukaryotic cell, comprising introducing two DNA sequences (I, II) into a cell, using an integrase (Int) to effect SSR. The invention also describes (I) a nucleic acid comprising a 243 base pair sequence (III), fully defined in the specification, or its derivatives; and (2) ector containing (III), or its derivatives, plus a therapeutic gene, or its derivatives. The method is particularly used in somatic gene therapy its derivatives. The archod is particularly used in somatic gene therapy transfer to animals, but can be applied more generally for gene therapy transfer to animal or plant cells. The method is simple and controllable, and provides stable and targeted integration of selected DNA sequences
                                                                       09
                                                                                            09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence-specific recombination of DNA in eukaryotes, useful particularly for somatic cell gene therapy, uses an integrase to effect recombination between att sites.
                                                                                                                                                                                                                                                                                                                          Sequence-specific recombination; SSR; integrase; gene therapy; somatic; targeted integration; attP; ds.
                                                                                TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                 Gaps
                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.0%; Score 160.4; DB 4; Length 243; 99.4%; Pred. No. 9.3e-25; ive 0; Mismatches 1; Indels 0;
                         Length 162;
                                                Indels
                                                                                                                                                        TATCATITIACGITICICGITICAGCITITITATACTAG 162
                                                                                                                                                                              TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 243 BP; 74 A; 34 C; 33 G; 102 T; 0 U; 0 Other;
 A; 22 C; 22 G; 75 T; 0 U; 0 Other;
                                                ·
0
                         DB 4;
                                    4.3e-25
                                             0; Mismatches
                        100.0%; Score 162; 100.0%; Pred. No. 4
                                                                                                                                                                                                                                                                                                    Bacteriophage lambda attP DNA fragment.
                                                                                                                                                                                                                                    AAF61418 standard; DNA; 243 BP.
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Best Local Similarity 99.4%;
Matches 161; Conservative
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                                              Conservative
   43
                                                                                                                                                                                                                                                                                                                                                            Bacteriophage lambda
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                                al Similarity
162; Conserv
  BP;
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 Sequence 162
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TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to a method for the site-specific integration of a DNA sequence into the plastid DNA of a plant or its derived cells. Transgenic plants in which a DNA sequence has been integrated, also their cell cultures, organs, tissues etc. are useful in human or animal nutrition, to produce seeds, and to produce pharmaceuticals or fine chemicals, e.g. enzymes, vitamins, amino acids, flavourings and aromatizing agents, dyes, antibodies and vaccines. The present sequence is a recognition sequence shown in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITIACAGIAITAIGIAGICIGITITITIAIGCAAAAICIAAITITAAIATATIGAIATITA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Site-specific integration of DNA into plastid DNA, useful for making transgenic plants used e.g. as food, by recombinase-mediated insertion.
                                                    TITIACAGIATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITIACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAAITIAAIATATATATATITA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sednence;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vegetable plastid transformation; transgenic, recognition seq
plant; site-specific integration; nutrition; seed production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinase lambda integrase attP DNA recognition sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                TAICATTTTACGTTCTCGTTCAGCTTTTTTTATACTAACTTG 162
                                                                                                                                                                                                            TATCATITIACGITICICGITICAGCITITITIATACTAGGITG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 248 BP; 76 A; 35 C; 34 G; 103 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 TATCATTTTACGTTCTCGTTCAGCTTTTTATACTAG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 160.4; DB 8;
Pred. No. 9.3e-25;
); Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 35; 164pp; German.
                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-DEC-2002; 2002WO-EP014303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.08;
                                                                                                                                                                                                                                                                                                                                                                 ACC85316 standard; DNA; 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemical production; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-541820/51.
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Best Local Similarity
Matches 161; Conserv
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126 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 167

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TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 

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us-10-082-772b-4.rng

TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATGTATTTTA 134

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core or several att sites, where an att site is heterologous to the corrownsome, and permits site-directed integration in the presence of larwockesion system (ACes) (II) comprising several sites that participate carporation system (ACes) (II) comprising several sites that participate in recombinase catalysed recombination, and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACE of molecule into an apation of artificial chromosome, preferably an ACE of molecule into an apation of transgenic animal (e.g. a fish, insect, reptile, amphibian, arachinid, or manumal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for comprising a library of ACes comprising random portions of a genome. ACC44612 committing a library of the program is necessarily and microcal in the accompanion of the comprising random portions of a genome and the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of t
                                                                                                                                                                                                                                                      Chromosome-based platform, artificial chromosome, eukaryotic chromosome, att site, integrase, recombinase, ACes, gene therapy, transgenic animal, platform artificial chromosome expression system, gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes a eukaryotic chromosome (I) comprising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lindenbaum M, Greene A, Leung J, Fleming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.0%; Score 160.4; DB 7; Length 282; 99.4%; Pred. No. 9.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 282 BP; 79 A; 49 C; 39 G; 115 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 207; 272pp; English.
                                                                                                                                                                                                      Murine rDNA PCR primer SEQ ID NO:72.
                              ACC44676 standard; DNA; 282 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-MAY-2002; 2002WO-US017452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2001; 2001US-0294758P
21-MAR-2002; 2002US-0366891P
                                                                                                                                             29-MAY-2003 (first entry)
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Best Local Similarity 99.49
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perez C, Li
Shellard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-140461/13.
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                                                                                                                                                                                                                                                                                                                                                                              musculus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perkins E,
Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                    ACC44676;
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ACC44676
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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes. The methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC comprises a heterologous incloid acid encoding a gene product or as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker proteins, lagands, receptors, ribozymes, therapeutic proteins, marker proteins, lagends, receptors, shipozymes, therapeutic proteins, and biopharmaceutical proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistence to diseases, insects, herbicides, or stress in a plant. The heterologous mucleic acid optionally encodes a product that alters agronomically important trait in the plant, e.g. a product that alters untrained use and/or improves the nutrient quality of the plant. The heterologous mucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (MAC). This product method for producing artificial chromosome (MAC). This producing artificial chromosome (PAC) artificial chromosome of the method for producing artificial chromosome of the method for producing artificial chromosome of the method for producing artificial chromosome of the method for producing and producing and producing of the plant of the method for producing and producing of the plant of the method for producing and produce represents an oligo relating to the method for producing and producing of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant of the plant 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    blood factor, herbicide, stress, agronomical, nutrient quality;
bacterial artificial chromosome, BAC, yeast artificial chromosome, YAC,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Plant artificial chromosome; PAC; transgenic plant; vaccine;
                                135 TATCATTTAGGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 176
TATCATTITACGITICICGITCAGCITITITITATACTAACTIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     producing plant artificial chromosomes of the invention
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                                                                                                                                                                                                                                                                                                                                                                 Artificial plant chromosome related oligo SEQ ID No 48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 263-264; 269pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Perkins
                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2001; 2001US-0294687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2002; 2002WO-US017451
                                                                                                                                                                                               ABT16636 standard; DNA; 282
                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AGRI-) AGRISOMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-140436/13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200296923-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
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                                                                                                                                                                                                                                                    ABT16636;
121
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TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG

Pred. No. 9.3e-25; 0; Mismatches 1; Indels

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ABQ80306 standard; DNA; 1469 BP.
                                                                                                        Lambda fragment in plasmid DNA.
                                                                                                                                                                                                                                      24-SEP-2002; 2002WO-JP009766.
                                                                                                                                                                                                                                                           25-SEP-2001; 2001JP-00291249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99.0%;
                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 99.4
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                             WPI; 2003-354676/33.
                                                                                                                                                                                                                                                                                    (DNAF-) DNAFORM KK.
                                                                                                                                                                                                                                                                                                RIKEN KK.
                                                                                                                                                                                       WO2003027991-A1
                                                                                                                                                                                                                                                                                                                      Hayashizaki Y;
                                                                                27-JUN-2003
                                                                                                                                                                                                               03-APR-2003
                                                                                                                                                                  Synthetic.
                                                           ABQ80306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61
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                                                                                                                                                                                                                                                                                                (RIKE)
            RESULT 7
                        ABQ80306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes a method of removing a transgene marker by flanking the transgene with a bacteriophage lambda attachment P (attP) region and inducing homologous recombination between attP regions so that the transgene is removed. This is useful in the production of transgenic plants with less risk of inter-species transmission of marker genes, which often encode proteins associated with, for example, herbicide and antibiotic resistance. The present sequence is the attP coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTTGATATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   258
                                               TITIACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAATITAATATATATATITA 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Removing a part of a transgene which has been integrated into a genome comprises inducing intrachromosomal homologous recombination between the attachment P regions of bacteriophage lambda flanking the transgene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09
                      74
             TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ritiacagnarrangracicigritirinangcaaarcraarraararangararra
TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                        Attachment P region; attP; recombination; marker gene removal; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 610 BP; 164 A; 108 C; 110 G; 228 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAGTTG 300
                                                                                                                135 TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAGTTG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAACTTG 162
                                                                                             TATCATTTTACGTTCTCGTTCAGCTTTTTTATACTAACTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.0%; Score 160.4; DB 5 99.4%; Pred. No. 9.3e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                Bacteriophage lambda attachment P region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 8; Fig 3D; 25pp; English.
                                                                                                                                                                            ВP
                                                                                                                                                                                                                                                                                                                                                                     15-SEP-2000; 2000WO-GB003543.
                                                                                                                                                                                                                                                                                                                                                                                            99GB-00021937
                                                                                                                                                                           AAF79770 standard; DNA; 610
                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 99.4
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-266072/27
                                                                                                                                                                                                                                                                                                                                                                                                                   (UYLE-) UNIV LEEDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Zubko E;
                                                                                                                                                                                                                                                                                                                       WO200121780-A2.
                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1999;
                                                                                                                                                                                                                         29-MAY-2001
                                                                                                                                                                                                                                                                                                                                             29-MAR-2001
                                                                                             121
                                                                                                                                                                                                                                                                                                                                                                                                                                         Meyer P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139
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                                                                     75
                                                                                                                                                                                                   AAF79770;
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                                                                                                                                                      RESULT 6
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The sequences given in ABQ80304-05 are primers which were used to amplify DNA for use in the material of the invention. The primers amplify a 1377 bp portion of lambda page DNA contained in a plasmid The amplified c sequence (ABQ80306) was attached to the printer material of the invention which comprises at least one support having at least one oligomer and/or colline applied on it. The printed material is useful in a method for synthesising DNA where the product of amplification and/or ligation is containation of nucleotide insertion/deletion, single nucleotide colline insertion/deletion, single nucleotide colline insertion/deletion, or SNP analysis.

CC cDNA and/or full-length cDNA which is recovered and used for determination of nucleotide insertion/deletion, or SNP analysis.

CC optionally, the cDNA and/or full-length cDNA is useful for the peptide, polymeptide or protein expression. The printed material is useful in crossarch applications, or for providing scientists with oligomer and/or polymers from the printed materials easily and immediately. From the printed materials easily and immediately and directly, without need to make a request for it. The oligomers and/or polymers and/or polymers and/or polymers and or printed material is a quick, efficient and labour and time while eliminating the need to use special equipment or inexpensive sample delivery system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITIACAGIATIATGIAGICTGITITITAIGCAAAAICTAATITAAIATATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Printed material useful as a delivery and storage system for oligomer and/or polymer, comprises a support having an oligomer and/or polymer applied on it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
Primer, PCR; amplify; lambda phage; printer material; insertion; deletion; single nucleotide polymorphism; sequencing; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 160.4; DB 7; Length 1469;
Pred. No. 9.2e-25;
0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 31-32; 91pp; English.
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ACC83020

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This sequence represents rat neuronal immediate early gene (IEG) cDNA clone R280. An IEG is a gene whose expression is rapidly increased immediately following a stimulus e.g., neuronal stimulation. Such neuronal IEGs have been found to encode a variety of proteins, including transcription factors, cytoskeletal proteins, growth factors and metabolic enzymes, as well as proteins involved in signal transduction. The identification of neuronal IEGs and the proteins they encode may provide important information about the function of neurons in, for example, learning, memory, synaptic transmission, tolerance and neuronal pasticity. Neuronal IEGs and antibodies against neuronal IEG proteins can be used to treat an animal with a deficiency in neuronal IEG proteins can be used to treat an animal with a deficiency in neuronal IEG responsivity deficiency may be a reduced or elevated level of expression of an IEC. The neuronal stimulus comprises a maximal electroconvulsive seizure and its effects influence learning or memory. The IEGs and protein products are useful in identifying compounds that modulate the expression or activity of IEG nucleic acids or proteins, respectively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel genes and polypeptides, useful for treating conditions related to a deficiency in nIEG responsiveness to a stimulus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           431 rererracaggicaeraanaceareraagragingaricaragigacigeanargriere 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITIACAGIAITAIGIAGICIGITITITAIGCAAAAICIAAITITAAIAITGAIAITIA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                               Immediate early gene; IBG; neuron; brain; function; growth factor; transcription factor; signal transduction; cytoskeletal protein; metabolic enzyme; learning; memory; synaptic transmission; tolerance; neuronal plasticity; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 1763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1763 BP; 478 A; 402 C; 452 G; 424 T; 0 U; 7 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 160.4; DB 2; Length Pred. No. 9.2e-25; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 TATCATTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATCATITIACGITICICGITICAGCITITITIATACTAG 162
                                          Rat neuronal immediate early gene cDNA clone R280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hiemisch H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE (BADI ) BASF-LYNX BIOSCIENCE AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 114-115; 134pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Goetz B,
                                                                                                                                                                                                                                                                                                                                                                                                         98US-0074518P.
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                                                                                                                                                                                                                                                                                                                                          99WO-US002462
                                                                                                                                                                                                                                                                                                                                                                                    98US-0074135P
05-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lanahan A,
Zhukovski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-590697/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                          05-FEB-1999;
                                                                                                                                                                                                                                                 WO9940225-A1
                                                                                                                                                                                                                                                                                                                                                                                    09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            L2-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Worley PF,
Nikolich K,
                                                                                                                                                                                                                                                                                             12-AUG-1999.
                                                                                                                                                                                                         sp.
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                                                                                                                                                                                                         Rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a method for storing and/or delivering an oligomer and/or polymer applied on support. The support has oligomer and/or polymer applied on it, and is in the form of loose-leaf sheet or a card. The support is useful for storing and/or delivering an oligomer and/or polymer applied on it. The present sequence is Bacteriophage lambda DNA used in the exemplification of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         808 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 867
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New support useful for storing and/or delivering an oligomer and/or polymer applied on support, has oligomer and/or polymer applied on it,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.0%; Score 160.4; DB 7; Length 1469; 99.4%; Pred. No. 9.2e-25; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                             Bacteriophage lambda DNA, SEQ ID NO:3 used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 1469 BP; 411 A; 300 C; 280 G; 478 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TAICATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 969
                         928 TATCATTTTACGTTCTCGTTCAGCTTTTTTTATACTAAGTTG 969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TATCATTITACGTTTCTCGCTTCAGCTTTTTTTATACTAACTTG 162
    121 TATCATTTTACGTTCTCGTTCAGCTTTTTTATACTAACTTG 162
                                                                                                                                                                                                                                                                                                                                          Oligomer storage; oligomer delivery; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 30-31; 70pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and a loose-leaf sheet or a card.
                                                                                                                                                          ACC83020 standard; DNA; 1469 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       05-NOV-2002; 2002WO-JP011492
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                                                                                                                                                                                                                                                      (first entry)
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es 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                    Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-441569/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DNAF-) DNAFORM KK. (HAYA/) HAYASHIZAKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKE ) RIKEN KK
                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2003040360-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hayashizaki Y;
                                                                                                                                                                                                                                                   27-AUG-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-2003.
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Scheek

Kuner R,

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Gaps

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ACC44716

AAZ30709/C ID AAZ3070 XX AC AAZ3070 XX

RESULT 9

Best\_Loca Matches

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ACC44716 standard; DNA; 4346 BP

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                                                                                                                                                  Chromosome-based platform, artificial chromosome, eukaryotic chromosome, att site, integrase, recombinase, ACes, gene therapy, transgenic animal, platform artificial chromosome expression system, gene, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4070 rererracadereactaaraceareraagracarearacaracaracararere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4130 TITIACAGIATTAIGIAGICIGITITITIAIGCAAAAICIAATTIAATATATTIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fleming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 U; 0 Other;
                                                                                                                   Plasmid pSV40193attPsensePUR nucleotide sequence SEQ ID NO:113.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Leung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99.0%; Score 160.4; DB 7, 99.4%; Pred. No. 9.2e-25; ive 0; Mismatches 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lindenbaum M, Greene A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 3; Page 244-245; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2002; 2002WO-US017452.
                                                                                                                                                                                                                                                                                                                                                                                                                    2001US-0294758P
                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAR-2002; 2002US-0366891P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 99.4%;
Matches 161; Conservative
                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perez C,
Shellard
                                                                                                                                                                                                                                        Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-140461/13
                                                                                                                                                                                                                                                                                                 WO200297059-A2
                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2001;
                                                                             29-MAY-2003
                                                                                                                                                                                                                                                                                                                                         05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Perkins E,
Stewart S,
                                                                                                                                                                                                                                                             Synthetic
                                     ACC44716;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interest
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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous introducing the PAC into a plant cell. Souch as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and proteins, ligands, receptors, ribozymes, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (MAC). This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4070 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 4129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Producing artificial chromosome by introducing a nucleic acid into plant
                                                                                                                                                                                                                                                                    Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4346 BP; 1022 A; 1208 C; 1094 G; 1022 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                  Artificial plant chromosome related plasmid DNA SEQ ID No 26.
4190 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACAGTTG 4231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 19; Page 255-256; 269pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perkins
                                                                                                                   BP.
                                                                                                                   ABT16615 standard; DNA; 4346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-MAY-2002; 2002WO-US017451.
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                                                                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AGRI-) AGRISOMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-140436/13.
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                                                                                                                                                                                                                                                                                                                                                                                                          WO200296923-A1
                                                                                                                                                                                              03-APR-2003
                                                                                                                                                                                                                                                                                                                                                                     Unidentified.
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                                                                                                                                                         ABT16615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Perez C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                              RESULT 11
                                                                                                 ABT16615
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02-AUG-2000; 2000WO-US021048.
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                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     partial/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *tag=
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                                                                                                                                                                                                                                                                                                                                                                                                                                            (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Vibrio harveyi.
Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-290731/30.
                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 P-PSDB; AAB20484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200127322-A2
coatings, etc
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                                                                                                                                                                                                                                                                                                                                                                                                                                          11-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19-APR-2001
                                                                                                161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -35_signal
                                                                                                                                                                                                                                                             121
                                                                                                                                                                                             19
                                                                                                                                                                                                                                                                                                                                                                                                            AAF30800;
                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric.
                                                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                                           SXS
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                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                             ਨੋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the complete nucleotide sequence of the plasmid Mallot This plasmid was used in the construction of the vector pFP510 which was used to express synthetic spider dragline variants, DP-1A.9 and DP-1B.9. pAl26i comprises a replication origin active in E. coli, a selectable genetic marker which is a gene conferring resistance to ampicillin, sites for the restriction endonucleases Bamil and BglII with no essential sequences between them, and a third restriction site for pst1, located within the selectable marker which produces cohesive ends incompatible with those produced by Bamil and BglII. The polypeptide monomers are variants based on a consensus sequence derived from the fibre forming regions of spider dragline protein, esp. the natural contein and the pattern of variation among individual repeats of DPI were designed to mimic the repeating consensus sequence of the natural protein and the pattern of variation among individual repeats. DP-1A consensus sequence which comprises four repeats which differ from the consensus sequence given in AAW06201, according to the pattern (1) (5): (1) the poly-alanine sequence is a langual and processed in a conting of the pattern (1) (5): (1) the poly-alanine sequence is a langual and processed in the pattern (1) (5): (1) the poly-alanine sequence is a langual and processed in the pattern (1) (5): (1) the poly-alanine sequence is a langual and processed in the pattern (2) when the entire poly-
               #130 TITTACAGIATTATGIAGTCTGTTTTTTATGCAAATCTAATTTAATATATTTA 4189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alanine sequence is deleted, so also is the surrounding sequence encompassing AGRGGLGGGGAANGG; (3) aside from the poly-alanine sequence, deletions usually encompass integral multiples of three consecutive residues; (4) deletion of GYG is generally accompanied by deletion of GRG in the same sequence; and (5) a repeat in which the entire poly-alanine acquence is deleted is generally preceded by a repeat containing six alanine residues. The proteins who be used to produce fibres of high tensile strength and elasticity, suitable for clothing, rope, surgical sutures, biomaterials for implants, plastic reinforcements, films,
                                                                                                                                                                                                                                                                                                        Spider; dragline protein; variant; monomer; polymer; circular;
lbre forming reglon; Spidroin 1; Nephila clavipes; DP1; mimic;
DP-1A analogue; fibre; high tensile strength; elasticity; clothing; rope;
surgical suture; implant; reinforcement; film; coating; ss.
New synthetic variants of spider dragline protein - for making fibres useful as clothing, surgical silk, plastic reinforcement etc., also related DNA, vectors and transformed cells.
                                                                                  4190 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 4231
                                                            TAICATTITACGITICICGITCAGCITITITITATACTAACTIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DUPO ) DU PONT DE NEMOURS & CO E I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 13; 168pp; English
                                                                                                                                                                         AAT18924 standard; DNA; 4909 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94WO-US006689.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93US-00077600
                                                                                                                                                                                                                                           17-JAN-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-036479/05
                                                                                                                                                                                                                                                                           Plasmid pA126i.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fahnestock SR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
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ID AAT18
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2516 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2457
                                                                                                                                                                                                                                                                                                                                            TITIACAGIATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTTGATATTTA 120
                                                                                                                                                                                 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Identifying a regulatory element capable of directing or regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF3; ds.
Sequence 4909 BP; 1216 A; 1251 C; 1258 G; 1184 T; 0 U; 0 Other;
                                                  99.0%; Score 160.4; DB 2; Length 4909; 99.4%; Pred. No. 9.2e-25; ive 0, Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               2396 TATCATTTTAGGTTTCTCGTTCAGCTTTTTTATACTAAGTTG 2355
                                                                                                                                                                                                                                                                                                                                                                                                                               TAICATTITACGITICICGTICAGCITITITATACTAACTIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vector plasmid pJMF3 encoding LacZ-chitobiase fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note= "lac repressor binding site"
1895. ,2014
/*tag= e
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        *tag= a
note= "CAP-cAMP binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Lac promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 function= "Lac promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     location/Qualifiers
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P-PSDB; AAB20484.
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Chimeric.
                         WO200127322-A2
                                                                                                        13-OCT-1999;
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21-JUN-2001
                                                   19-APR-2001
                                                                                                                                                          Zyskind J;
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                                                                                                                                                                                                                                                                                                                                                                                                                             4822
                                                                                                                                                                                                                                                                                                                                                                        4703 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 4762
                                                           The present sequence is that of vector plasmid pJMF3, which includes phage lambda attP and the lac promoter with the first 21 amino acids of lacZ-alpha (from plasmid pUC19) fused in-frame to the Vibrio harveyi chicobiase gene (see AAB20484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as reporter. A claimed reporter gene construct comprises pJMF3. The invention also comprises expression vectors which express the cytoplasmic form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory alement capable of directing and regulating transcription within a test sequence; detecting a successful transformation; and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactossidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter activity.
                                                                                                                                                                                                                                                                                                                                                                                                  TITIACAGIATTAIGIAGICIGITITITIAIGCAAAAICIAAITIAAIAITIGAIAITIA 120
transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                               09
                                                                                                                                                                                                                                                                                                                                                                                                                   4763 TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                               TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chitobiase; reporter gene; LacZ gene; promoter; vector; pJMF4; ds.
                                                                                                                                                                                                                                                                                                                       ;
0
                                                                                                                                                                                                                                                                  Sequence 5641 BP; 1539 A; 1305 C; 1336 G; 1461 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                          Score 160.4; DB 4; Length 5641; Pred, No. 9.2e-25;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TATCATTITACGITICTCGGTTCAGCTTTTTTATACTAAGTTG 4864
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TATCATITITACGITICICGTICAGCITITITATACTAACTIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vector plasmid pJMF4 encoding LacZ-chitobiase fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note= "Lac repressor binding site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note = "CAP-cAMP binding site"
                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  function= "Lac promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            function= "Lac promoter"
                                      Example 1; Page 32-34; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.0%;
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 99.4
Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       121
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phage lambda attP and the lac promoter with the first 21 amino acids of lacZ-alpha (from plasmid puCl9) fused in-frame to the Vibrio harveyi chitobiase gene (see AAE20484). The invention relates to genetic constructs and methods of using a cytoplasmic form of chitobiase enzyme as a reporter. A claimed reporter gene construct comprises pUMF4. The invention also comprises expression vectors which express the cytoplasmic form of chitobiase. Methods are provided for: characterizing a promoter; form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transformation, and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene in that it is not necessary to engineer many host cells to lack reporter gene in that it is (Updated on 11-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITIACAGIATIAIGIAGICIGITITITIAIGCAAAAICIAAITIAAIAIATIGAIATITA 4922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAAATATATTGATATTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence is that of vector plasmid pJMF4, which includes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chitobiase; reporter gene; dnaA gene; promoter; vector; pDYK9; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5670 BP; 1567 A; 1302 C; 1356 G; 1445 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 160.4; DB 4; Length 5670; Pred. No. 9.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vector plasmid pDYK6 encoding chitobiase reporter enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAACTTG
/product= "lacZ-chitobiase fusion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 34-36; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99.0%;
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                                                                                                                                                                                                                                                02-AUG-2000; 2000WO-US021048
                                                                                                                                                                                                                                                                                                                       99US-0159221P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                      (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (revised)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-290731/30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
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The present sequence is that of vector plasmid pDYK9, which comprises the Vibrio harveyi chitobiase gene under the control of the Escherichia coli duaA promoter in plasmid pACYC184. pDYK9 was used to assess the regulation of the daaA gene using chitobiase as a reporter enzyme. A claimed reporter gene construct comprises pDYK9. The invention relates to enzyme as a reporter. The invention also comprises expression vectors which express the cytoplasmic form of chitobiase which express the cytoplasmic form of chitobiase. Methods are provided for: characterizing a promoter; identifying a regulatory element capable of directing and regulating transformation; and for monitoring the activity of a promoter. Chitobiase has an advantage over beta-galactosidase as a promoter. Chitobiase has an advantage over beta-galactosidase as a reporter gene system in that it is not necessary to engineer many host cells.
                                                                                                                                                                                                                                                                                               Identifying a regulatory element capable of directing or regulating transcription (e.g. a promoter) comprises providing a construct linked to a nucleic acid encoding a cytoplasmic form of chitobiase.
                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 29-30; 44pp; English.
                                                                                                02-AUG-2000; 2000WO-US021048.
                                                                                                                                       99US-0159221P
                                                                                                                                                                              (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                            WPI; 2001-290731/30
                      WO200127322-A2.
                                                                                                                                       13-OCT-1999;
                                                           19-APR-2001
                                                                                                                                                                                                                     Zyskind J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              field)
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Sequence 5826 BP; 1574 A; 1346 C; 1389 G; 1517 T; 0 U; 0 Other; Query Match 99.0%; Score 160.4; DB 4; Length 5826; Best Local Similarity 99.4%; Pred. No. 9.2e-25; Matches 161; Conservative 0; Mismatches 1; Indels 0;

o;

Gaps

0;

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1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG

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Search completed: September 9, 2004, 18:05:41 Job time: 185.482 secs

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Sequence 174, Applisequence 4, Applisequence 17, Applisequence 173, Applisequence 173, Applisequence 14, Applisequence 8, Applisequence 8, Applisequence 72, Applisequence 72, Applisequence 72, Applisequence 72, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 15, Appl
Sequence 9, Appli
                                                                 9, 2004, 19:34:38; Search time 128.856 Seconds (without alignments) 3982.858 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 57,
Sequence 57,
Sequence 57,
                                                                                                                          102
1 ctgcttttttatactaagtt......taaaatcattatttgatttc 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description
                                                                                                                                                                                                                                                                                                                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-403-232-173
US-10-310-695-14
US-10-310-695-14
US-10-627-711-8
US-10-161-403-72
US-99-244-805-57
US-99-244-805-57
US-10-792-481-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7 US-10-310-695-15
7 US-10-627-711-9
8 US-10-403-232-174
9 US-10-432-188-4
US-09-970-921-7
US-09-970-921-10
                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                    3304383 seqs, 2515761380 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                          Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                               Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                  US-10-082-772B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length DB
                                                                                                                                                                 IDENTITY NUC
                                                                     September
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match ]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.4
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100.4
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                                                                                                                                           Sequence:
                                                                                                                                                                                                                                                                                                                                  Database
                                                                     Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               υυυ
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Sequence 8, Appli Sequence 13, Appli Sequence 113, Appl Sequence 10, Appl Sequence 20, Appl Sequence 41, Appl Sequence 41, Appl Sequence 34, Appl Sequence 37, Appl Sequence 42, Appl Sequence 42, Appl Sequence 45, Appl Sequence 46, Appl Sequence 47, Appl Sequence 48, Appl Sequence 48, Appl Sequence 36, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appl Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli	equence 177 equence 395 equence 186 equence 90, equence 70, equence 71, equence 71,
US-10-270-176-8 US-10-270-176-3 US-10-270-176-3 US-10-161-403-113 US-10-270-176-30 US-10-270-176-30 US-10-270-176-40 US-10-270-176-40 US-10-270-176-40 US-10-270-176-40 US-10-270-176-40 US-10-270-176-37 US-10-270-176-37 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-38 US-10-270-176-19	10-301-849A- 10-374-780A- 10-151-10-10-10-10-10-10-10-10-10-10-10-10-10
	112333333333333333333333333333333333333
2953 3663 3695 3695 44346 47346 5646 5771 5771 5771 5771 5771 5771 5771 577	100 1688 2717 100 659 2591 2607 2831
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	000000000
	00000000000000000000000000000000000000
11 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	000 0000 0000444444 00001100040

## ALIGNMENTS

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Sequence 15, Application US/10310695
Publication No. US20040110293A1
GENERAL INFORMATION:
APPLICANT: DROGE, PETER
APPLICANT: ENENKEL, BARBARA
TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
FILE REPERENCE: DEBE: 01908
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 CIGCITITITATACTAGGITGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                        Length 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 102; DB 17;
100.0%; Pred. No. 1.6e-18;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 102; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
RESULT 1
US-10-310-695-15
                                                                                                                                                                                                                                                                 SEQ ID NO 15
TENGTH: 102
                                                                                                                                                                                                                                                                                                                                                                US-10-310-695-15
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    g
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## 61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102 61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102 ; Sequence 9, Application US/10627711; Publication No. US20040115812A1; GENERAL INFORMATION: RESULT 2 US-10-627-711-9 ò

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2398 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCCATTGCTTATCAATTTGTTGCAACG 2457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 CIGCITITITATACTAAGTIGGCATTATAAAAAAAGCATIGCTTATCAATTIGTIGCAACG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "T-DNA of pTTS243"

NAME/KEY: misc_feature

LOCATION: Complement(1)..(25))

OTHER INFORMATION: label = RB, "T-DNA right border"

NAME/KEY: misc feature

LOCATION: Complement(199)..(331))

OTHER INFORMATION: label = 3'97, "region containing 3' untranslated OTHER INFORMATION: end of Agrobacterium T-DNA gene 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature 1
LOCATION: Complement(1884)..(2258))
OTHER INFORMATION: label = P35S, "35S promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature [...]
LOCATION: complement((332)..(883))
OTHER INFORMATION: label = bar, "region coding for phosphinthricin OTHER INFORMATION: acetyl transferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 3049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2458 AACAGGICACIAICAGICAAAAIAAAAICAITATITGAIIIC 2499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (228T)...(3969)
OTHER INFORMATION: label = PE1, "promoter of E1 gene of 1
OTHER INFORMATION: 92/13956)"
NAME/KEY: misc. feature
LOCATION: (3970)..(4245)
OTHER INFORMATION: label = synb*; "improved barstar DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 AACAGGICACTAICAGICAAAAIAAAAICAITAITIGAITIC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 102; DB 13;
100.0%; Pred. No. 5.1e-18;
rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 7. Application US/09970921
Patent No. US20020133845A1
GENERAL INFORMATION:
TELL OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2428-0108P
CURRENT APPLICATION NUMBER: US/09/970,921
NUMBER OF SEQ ID NOS: 10
SEQ ID NO 7
CURRENT APPLICATION NUMBER: US/10/432,148
CURRENT FILING DATE: 2003-05-16
NUMBER OF SEQ ID NOS: 4
SEQ ID NO 4
LENGTH: 3049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.
Matches 102; Conservative
                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: mRNA
LOCATION: (2928)..(3049)
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: TATA signal LOCATION: (2877)..(2883)
                                                                                                                                                                                          ORGANISM: Beta vulgaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc feature LOCATION: (2281) .. (396)
                                                                                                                                                                                                                                           NAME/KEY: promoter LOCATION: (1)..(2998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-09-970-921-7/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 5349
                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-432-148-4
                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     à
APPLICANT: YANG, Shuwei
TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
TITLE OF INVENTION: SCREENING OF CDNA CLONES
FILE REPERBACE: 51236US
CURRENT PILING DATE: 2003-07-28
PRIOR APPLICATION NUMBER: US/10/627,711
PRIOR APPLICATION NUMBER: 06/398,589
PRIOR PILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PATCHIL VERSION 3.2
SOFTWARE: PATCHIL VERSION 3.2
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Publication No. US20030226164A1
GENERAL INFORMATION:
BURDICANT: Suttie, Janet Louise
APPLICANT: Suttie, Janet Louise
APPLICANT: Guideng
APPLICANT: Que, Qiudeng
APPLICANT: de Framond, Anic
TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
FILE REFERENCE: 70005USPS
CURRENT APPLICATION NUMBER: US/10/403,232
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 185
SOFTWARE: PatentIn version 3.2
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100.0%; Pred. No. 1.6e-18;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1.6e-18;
ive 0; Mismatches 0;
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Publication No. US20040064853A1
GENERAL INFORMATION:
APPLICANT: KWS SAAT AG
APPLICANT: KWS SAAT AF
FILLE OF INVENTION: tissue specific promoter
FILE REFERENCE: tissue specific promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Bacteriophage lambda
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Matches 102; Conservative
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Matches 102; Conservative
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                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial
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US-10-432-148-4
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LENGTH: 243
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LOCATION: Complement ((318)..(869))
OTHER INFORMATION: label = bar, "region coding for phosphinothricin
OTHER INFORMATION: acetyl transferase"
NAME/KEY: misc feature
LOCATION: Complement ((870)..(1702))
OTHER INFORMATION: Upbel = P355, "355 promoter of Cauliflower Mosaic
OTHER INFORMATION: Virus"
NAME/KEY: misc feature
LOCATION: (1710)..(284)
OTHER INFORMATION: label = PTA29, "promoter of TA29 gene of Nicotiana
OTHER INFORMATION: tabacum"
                                                                                                                                                                                                                                                                                             0; Gaps
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INFORMATION: label = 3'chs, "region containing 3' untranslated INFORMATION: end of chalcone synthase gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Artificial Sequence: other nucleic OTHER INFORMATION: acid, "plasmid pLH48"
NAME/KEY: misc feature
LOCATION: Complement((39)..(317))
OTHER INFORMATION: label = 3'nos, "region containing 3' untranslated OTHER INFORMATION: end of nopaline synthase gene of Agrobacterium OTHER INFORMATION: T-DNA"
                   COGNION: (4246)..(4577)
COTHER INFORMATION: label = 3'chs, "region containing 3' untranslated OTHER INFORMATION: end of chalcone synthase gene"
NAME/KEY: misc_feature
COMPLEMENTION: Complement((5325)..(5349))
COTHER INFORMATION: label = LB, "T-DNA left border"
US-09-970-921-7
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; Pred. No. 6.2e-18;
0; Mismatches 0; Indels 0
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LOCATION: (2285). (2560)
OTHER INFORMATION: label = synb*, "improved barstar DNA"
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TITLE OF INVENTION: Improved Barstar Gene
FILE REFERENCE: 2428-0108P
CURRENT APPLICATION NUMBER: US/09/970,921
CURRENT FILING DATE: 2001-10-05
SOFTWARE: PAtentin Ver: 2.0
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100.0%;
Best Local Similarity 100.0%;
Matches 102; Conservative 0
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NAME/KEY: misc feature
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LENGTH: 5611
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APPLICANT: BRENKEL, BARBARA
TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
FILE REFERENCE: DEBE: 01902
CURRENT APPLICATION NUMBER: US/10/310,695
CURRENT PILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 2
3200 CTGCTTTTTTATACTAAGTTGGCATTATAAAAAGCATTGCTTATCAATTTGTTGCAACG 3141
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US-10-403-232-173
Sequence 173, Application US/10403232
Publication No. US20030226164A1
GENERAL INFORMATION:
APPLICANT: Suttie, Janet Louise
APPLICANT: Chilton, Mary-Dell
APPLICANT: Que, Qiudeng
APPLICANT: Que, Qiudeng
APPLICANT: Que, Cambination In Plants
FILE REFRENCE: 70005USPS
CURRENT APPLICATION NUMBER: US/10/403,232
CURRENT APPLICATION NUMBER: US/203-28
NUMBER OF SEQ ID NOS: 185
SOFTWARE: Patentin version 3.2
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Pred. No. 5.9e-18;
0; Mismatches 1; Indels
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Pred. No. 5.9e-18;
0; Mismatches 1; Indels
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                                                         61 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 102
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Publication No. US20040110293A1
GENERAL INFORMATION:
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Best Local Similarity 99.0%;
Matches 101; Conservative
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Best Local Similarity 99.0%;
Matches 101; Conservative
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US-09-244-805-57/c
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Publication No. US20040115812A1
GENERAL INPORMATION:
SENERAL INPORMATION:
STATE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND
TITLE OF INVENTION: SCREENING OF CDNA CLONES
                                                                                                                                                                  Sequence 14, Application US/10310695
Publication No. US20040110293A1
GENERAL INFORMATION:
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    202 AACAGGICACIAICAGICAAAAIAAAAICAIIAIIIIGAIIIC 243
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CURRENT APPLICATION NUMBER: US/10/627,711
CURRENT FILING DATE: 2003-07-28
FRIOR APPLICATION NUMBER: 60/398,589
PRIOR FILING DATE: 2002-07-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn version 3.2
LENGTH: 248
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ORGANISM: Bacteriophage lambda
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Best Local Similarity 99.0%;
Matches 101; Conservative (
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Best Local Similarity 99.0%
Matches 101; Conservative
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                                                                                                                 RESULT 9
US-10-310-695-14
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RESULT 11 US-10-161-403-72

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156 CAGCTTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 215
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APPLICANT: Worley, Paul F.
APPLICANT: Landan, Anthony
APPLICANT: Landan, Anthony
APPLICANT: Jandan, Anthony
APPLICANT: Goetz, Bernard
APPLICANT: Scheek, Sigrid
APPLICANT: Kner, Rohini
APPLICANT: Scheek, Sigrid
APPLICANT: Scheek, Sigrid
APPLICANT: Stheokoski, Eugene
TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
TITLE OF INVENTION: 1996-02-05
TITLE REFERENCE: 10496/004001
CURRENT APPLICATION NUMBER: 60/074,518
EARLIER PILING DATE: 1999-02-05
EARLIER PLING DATE: 1998-02-05
SARLIER PLING DATE: 1998-02-05
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FASISEQ for Windows Version 4.0
FENCINE APPLICATION NUMBER: 60/074,135
SARLIER FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 62
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                                                                                                                                                                                                                                       APPLICANT: Leung, DUSEPALLING
APPLICANT: Fleming, Elena
APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE BEFERRNCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
FRIOR APPLICATION NUMBER: 60/294,758
FRIOR FILING DATE: 2002-03-01
FRIOR PLING DATE: 2002-03-01
FRIOR PLING DATE: 2002-03-01
FRIOR PLING DATE: 2002-03-01
FRIOR FILING DATE: 2002-03-01
Sequence 72, Application US/10161403 Publication No. US20030119104A1 GENERAL INFORMATION: APPLICANT: Perkins, Edward
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Publication No. US20030203840A1
                                                                                                                                                        Lindenbaum, Michael
Greene, Amy
Leung, Josephine
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Best Local Similarity 99.0%
Matches 101; Conservative
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US-10-161-403-72
                                                                                                                                   Perez, Carl
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FEATURE:
NAME/KEY: misc feature
LOCATION: (1)...(1763)
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LENGTH: 1763
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Publication No. US20030211984A1
GENERAL INFORMATION:
APPLICANT: Worley, Paul F.
APPLICANT: Lanahan, Anthony
TITLE OF INVENTION: IMMEDIATE EARLY GENES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: JHUL530-3
CURRENT FILING DATE: 1999-02-05
FRICK APPLICATION NUMBER: 06/074,518
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-12
PRIOR FILING DATE: 1999-02-06
NUMBER OF SEQ ID NOS: 63
NUMBER OF SEQ ID NOS: 63
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                       Query Match 98.4%; Score 100.4; DB 11; Length 1763; Best Local Similarity 99.0%; Pred. No. 1.2e-17; Matches 101; Conservative 0; Mismatches 1; Indels 0;
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APPLICANT: Lanahan, Anthony
APPLICANT: Goetz, Bernard
APPLICANT: Heimisch, Holger
APPLICANT: Kuner, Rohini
APPLICANT: Scheek, Sigrid
APPLICANT: Nikolich, Karoly
APPLICANT: Zhukovski, Eugene
TITLE OF INVENTION: IMMEDIATE BARLY GENES AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                              230 AACAGGTCACTATCAGTCAAAATAAAATCATTATTTGATTTC 189
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; Publication No. US20040152658A1
; OTHER INFORMATION: y = C or T; OTHER INFORMATION: n = A, T, C or G US-09-244-805-57
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OTHER INFORMATION: y = C or T
OTHER INFORMATION: n = A,T,C or G
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ORGANISM: Eukaryote
FEATURE:
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SEQ ID NO 57
LENGTH: 1763
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1082 CAGCTTTTTATACTAAGTTGGCATTATAAAAAAGCATTGCTTATCAATTTGTTGCAACG 1141
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APPLICANT: Haldimann, Andreas
TITLE OF INVENTION: PLASMIDS, STRAINS, AND METHODS OF USE
FILE REPERCE: 290.00140101
CURRENT APPLICATION NUMBER: US/10/270,176
CURRENT PILING DATE: 2002-10-10
PRIOR PILING DATE: 2001-10-10
PRIOR APPLICATION NUMBER: 60/328,642
PRIOR FILING DATE: 2001-10-10
PRIOR FILING DATE: 2002-04-24
NUMBER OF SEQ ID NOS: 118
SOGTWARE: Patentin version 3.0
SEQ ID NOS
TENNING: 2002-04-24
SEQ ID NOS: 118
SEQ ID NOS: 118
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TITLE OF INVENTION: THEREFOR
FILE REFERENCE: 10496/004001
CURRENT APPLICATION NUMBER: 02/10/792,481
CURRENT FILING DATE: 2004-03-02
PRIOR APPLICATION NUMBER: US/09/244,805
PRIOR PILING DATE: 1999-02-05
PRIOR PILING DATE: 1999-02-12
PRIOR PRICATION NUMBER: 60/074,518
PRIOR PELING DATE: 1998-02-12
PRIOR APPLICATION NUMBER: 60/074,135
PRIOR FILING DATE: 1998-02-06
NUMBER OF SEQ ID NOS: 62
SOFTWARE: FRACESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(1763)
OTHER INFORMATION: y = C or T
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 99.0%;
Matches 101; Conservative (
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Search completed: September 10, 2004, 00:14:08 Job time : 129.856 secs

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1 tctgttacaggtcactaata.....agcttttttatactaacttg 162
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1: /cgn2 6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2 6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2 6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2 6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-453-702B-66
US-08-01-667A-18
US-08-710-544-18
US-08-785A-18
US-09-790-988-1
US-09-790-988-1
US-09-790-988-1
US-09-790-988-1
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US-10-204-708-88
US-08-961-527-245
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US-08-021-667A-17
US-08-410-544-17
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US-10-204-708-33
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Maximum Match 1008
Listing first 45 summaries
                                            sw model
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Gapop 10.0 , Gapext 1.0
                                           - nucleic search, using
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Maximum DB seq length: 200000000
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Match Length DB
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19124
640681
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5455
10467
1725
6326
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160.4
104.6
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97.4
67.8
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61.4
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37.6
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36.4
36.4
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                                            OM nucleic
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Perfect
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Sequence 24, Appl
Sequence 856, Appl
Sequence 151, Appl
Sequence 151, Appl
Sequence 834, Appl
Sequence 1, Appli
Sequence 24, Appl
Sequence 21, Appl
Sequence 21, Appl
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Sequence 118, App
Sequence 8, Appli
Sequence 39, Appl
Sequence 2779, Ap
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Sequence 5, Appli
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Sequence 2
Sequence 8
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Sequence 78, Application US/08556978B
Patent No. 6568169
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
TITLE OF INVENTION: SPIDER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 WARKET STREET
CITY: WILMINTON
STATE: DELAWARE
COUNTRY: UNITED STATES OF AMERICA
ZIP: 19898
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match 99.0%; Score 160.4; DB 3; Best Local Similarity 99.4%; Pred. No. 1.6e-28; Matches 161; Conservative 0; Mismatches 1;
US-08-340-820-24
US-08-593-535-24
US-09-976-594-856
US-10-204-708-22
US-08-916-421B-1
US-08-956-171E-834
US-09-956-171E-834
US-09-807-258-21
US-09-807-258-21
US-09-807-258-21
US-09-807-258-21
US-09-807-258-21
US-09-807-258-21
US-09-807-258-21
US-09-134-008-8
US-09-134-008-2779
US-09-134-008-2779
US-09-134-008-2779
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COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
FILING DATE: US/08/556,978B
FILING DATE: US/08/556,978B
FILING DATE: UNBER: US/08/556,978B
ATTORNEY/AGRIT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REGISTRATION NUMBER: 33,692
REFERENCE/DOCKET NUMBER: 33,692
REFERENCE/DOCKET NUMBER: 33,692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4909 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                     1664976
998
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STRANDEDNESS: single
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US-08-556-978B-78/c
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1 TCTGTTACAGGTCACTAATACCATCTAAGTTGATTCATAGTGACTGCATATGTTGTG

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APPLICATION NUMBER: US/07/590,988A
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                             FILING DATE: 19901001
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Nicholas J. Seay
REGISTRATION NUMBER: 27,386
REFERRINCE/DOCKET NUMBER: 9629
TELECOMMUNICATION INFORMATION:
TELECHONE: (608) 251-5000
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Welch, Rod
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Best Local Similarity 99.4
Matches 161; Conservative
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COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ANTI-SENSE: no
US-07-590-988A-1
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                                                                    61 TITIACAGTAITATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTG
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Patent No. 6620585
GENERAL INFORMATION:
TITLE OF INVENTION: USE OF ECTOENZYMES AND SECRETED ENZYMES
TITLE OF INVENTION: TO MONITOR CELLULAR PROLIFERATION
FILE REFERENCE: ELITRA.012A
CURRENT APPLICATION NUMBER: US/09/630,929
CURRENT FILING DATE: 2000-08-02
                                                                                                                                                                                                                                                  2396 TATCATTTTACGTTTCTCGTTCTAGCTTTTTTTATACTAAGTTG 2355
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                                                                                                                                                                                                              121 TATCATTTTACGTTCTCGTTCAGCTTTTTTATACTAACTTG 162
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STREET: FIRST WISCONSIN PLAZA
CITY: MADISON
STRTE: WISCONSIN
STRTE: WISCONSIN
COUNTRY: U.S.A.
ZIP: 53701
COMPUTER READBLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFFWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
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99.4%; Pred. No. 1.6e-28;
live 0; Mismatches 1;
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Patent No. 5227288
GENERAL INFORMATION:
ALBATORE, THORMATION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE:
CORRESSEE:
C
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 6043
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Matches 161; Conservative
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US-09-630-929-4/c
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5933 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                 Length 7652;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch. 1.44Mb storage
                                                                                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TATCATITIACGITICICGITICAGCITITITIATACIAAGTIG 6094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TATCATTTTACGTTTCTCGTTCAGCTTTTTTTTATACTAG 162
                                                                                                                                                                                                                                                                                                                                                 Score 160.4; DB 1;
Pred. No. 1.6e-28;
0; Mismatches 1;
TELEAX: (608) 251-9000
TELEAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7652 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: synthetic recombinant plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARRS: WOR'D FATECT 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/453,702B
FILING DATE: 03-Dec-1999
CLASSIFICATION: «Unknown>
PRIOR APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: SGAY, NICHOLAS J.
REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
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Gaps

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102 TCTGTTACAGGTCACTAATACCATCTAAGTAGATTGATTCATAGTGACTGCATCTGTTGTG 161
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                                                                                                                                                                1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 17, Application US/08410544

Patent No. 5607646

GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE FREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 200;
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                                                                                                                                                                                                                                                                                      162 TITIACAGIAITAIGIAGICIGITITITIAIGCAAAAICT 200
                                                                                                                                                                                                                                                             61 TITIACAGIAITAIGIAGICIGIITITITAIGCAAAAICI 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOBDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Rolease #1.0, Version #1.25
GURRENT APPLICATION DATR:
APPLICATION NUMBER: US/08/410,544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.1%; Score 97.4; DB 1;
99.0%; Pred. No. 3.1e-14;
iive 0; Mismatches 1;
                                                                            Score 97.4; DB 1;
Pred. No. 3.1e-14;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Antonelli, Terry, Stout & Kraus STREET: Suite 600, 1919 Pensylvania Ave., NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
REFERENCE/DOCKET NUMBER: 520.31930X00
TELECOMMUTCATION INFORMATION:
TELEPHONE: 202-828-0300
TELEFAX: 202-828-0380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                 60.1%;
99.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity 99.0
98, Conservative
                                                                                                                               Conservative
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CORRESPONDENCE ADDRESS:
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                                                                                   Query Match
Best Local Similarity
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HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20006
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                  ; ANTI-SENSE:
US-08-021-667A-17
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US-08-410-544-17
                                                                                                                             98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TITIACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTTGATATTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLYNUCLEOTIDE CAPTURING TIP AND POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION METHOD USING SAME
                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                Length 38584;
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CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/021,667A

FILING DATE: 1993024

CLASSIFICATION: 435

ATTORIEY/AGENT INFORMATION:

NAME: TELEY, David T.

REGISTRATION NUMBER: 20,178

REGISTRATION NUMBER: 520.31930X00

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEFAX: 202-828-0300

TELEFX: 440280/248545

INFORMATION FOR SEQ ID NO: 17:

SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 17, Application US/08021667A

Sequence 17, Application US/08021667A

Patent No. 5434049

GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE MET
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pennsylvania Ave., NW
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                Score 104.6; DB 4;
Pred. No. 9.9e-16;
0; Mismatches 24;
REFERENCE/DOCKET NUMBER: 960296.95017
                                                                                                                                                                                                              ; SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-453-702B-50
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                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
                                                                                                                             LENGTH: 38584
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 83.2%;
Matches 119; Conservative
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
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Best Local Similarity
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US-08-021-667A-17
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Patent No. 6365723
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                                                                                                                                                                                                                                                                                                                           Sequence 17, Application US/08728785A
Patent No. 5817506
GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: DOLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 referración de la reconstrucción de la reconstr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
CITY: Arlington
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/728,785A
FILNG DATE: 10-OCT-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/410,544
FILNG APPLICATION NUMBER: 08/410,544
FILNG DATE: 21-MAR-1995
PRIOR APPLICATION NUMBER: 08/21,667
FILNG DATE: 44-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: FLELNG DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: TEATY, DAVIG T.
                                                                                           162 TTTTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCT 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rrrracagrarrargragrergrrrrrargcaaaarcr 200
                                61 TITTACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCT 99
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ER: 520.31930X00
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6600
TELEFAX: 703-312-6600
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 200 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Best Local Similarity
Matches 98; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE: NO
US-08-728-785A-17
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                                                                                                                                                                                                                                                                                  US-08-728-785A-17
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RESULT 8 US-09-453-702B-66/c ; Sequence 66, Application US/09453702B

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60 GITTIACAGIATTATGIAGICIGITITITATGCAAAATCIAATTIAATATATATATTT 119
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                          41.9%; Score 67.8; DB 4; Length 9827; 69.0%; Pred. No. 2.3e-07; trive 0; Mismatches 47; Indels 1
                                                                                                            TITLE OF INVENTION: No. 6365723el Sequences of E. NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
CITY: Madison
STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 ATAICATITIACGITICICGITCAGCITITIAIA 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 960296.95017
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
TELEFAX: (608) 251-9166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-09-453-702B-66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-021-667A-18

Sequence 18, Application US/08021667A

Sequence 18, Application US/08021667A

GENERAL INFORMATION:
APPLICANT: OKANO, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CF
TITLE OF INVENTION: POLYNUCLEOTIDE FITTLE OF INVENTION: METHOD USING SAN NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick
                                                           Nicole T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 66
SEQUENCE CHARACTERISTICS
                                                         Perna,
Plunkett, Guy
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Matches 107; Conservative
                                         Burland,
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Arlington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Arling STATE: VA COUNTRY: US/ ZIP: 22209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     % Sequence 18, Application US/08410544

; Sequence 18, Application US/08410544

; Patent No. 5607646

; GENERAL INFORMATION:
    APPLICANT: Kambara, Hideki

; TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
    TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
    TITLE OF INVENTION: METHOD USING SAME

; UNMERS OF SEQUENCES: 18
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Antonelli, Terry, Stout & Kraus

; STREET: Suite 600, 1919 Pensylvania Ave., NW

CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  37.9%; Score 61.4; DB 1; Length 201; 98.4%; Pred. No. 5.1e-06; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: DC
COUNTRY: USA
ZIP: 20006
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/410,544
                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,667A
FILING DATE: 19930224
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus STREET: Suite 600, 1919 Pennsylvania Ave., NW CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 520.31930X00
TELECOMMUNICATION INVERMATION:
TELEPHONE: 202-828-0380
TELEEX: 440280/248545
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             FILING DATE: 19930224
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Terry, David T.
REGISTRATION NUMBER: 20,178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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US-08-021-667A-18
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                                                                                                                                20006
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PRIOR APPLICATION: 435

PRIOR APPLICATION: 435

PRIOR APPLICATION ONTH: 42-82-393

PULLAND DATE: 24-82-393

PULLAND DATE: 27-82-393

PULLE TYPE: DAM (Genomic)

PULLE TYPE: DAM (Genomic)

PULLE TYPE: DAM (Genomic)

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PULLE TYPE: DAM
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143 AGCTTTTTTATACTAACTT 161
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.6%;
54.7%;
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23.69
Best Local Similarity 54.75
Matches 76; Conservative
                                                                                                                                                                                                                                                                                                                                 STREET: 620 Newcort
CITY: Newport Beach
CTATE: California
                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS: ADDRESSE: Knobbe Ma.
                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA UVBOTHRTICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 92660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE:
US-08-487-826B-13
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US-09-790-988-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 TTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTATA 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 TGTIACAGGICACIAAIACCAICTAAGTAGTIGATICAIAGIGACIGCAIAIGIIGIGIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WAITANABE, HIDEAT
APPLICANT: WAITANABE, HIDEAT
APPLICANT: HATTORI, WASAHHRA
APPLICANT: ARAZAHIRA
TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0129
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT PILING DATE: 2001-02-23
PRIOR PILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PALENTH OF SEQ ID NOS: 7
SOFTWARE: PALENTH OF SEQ ID NOS: 7
SOFTWARE: PALENTH OF SEQ ID NOS: 7
SOFTWARE: PALENTH OF SEQ ID NOS: 7
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SOFTWARE: PALENTH OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 AATTTAATATATTGATATTTATATCATTTTACGTTTCCGTTCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         160560 ATAATATTTTTTCAGTATATTCATTAATATTGTTTT 160598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   37.9%; Score 61.4; DB 1;
98.4%; Pred. No. 5.1e-06;
live 0; Mismatches 1;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-312-6666
FORMATION: 703-312-6666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 13
US-08-487-825B-13/c
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09790988
Patent No. 6632935
                                                                                                                                                                                                                                                           TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 98.4º
Matches 62, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          ; ANTI-SENSE:
US-08-728-785A-18
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APPLICANT: Sim, Kim L.
APPLICANT: Chitnis, Chetan
APPLICANT: Chitnis, Chetan
APPLICANT: Miller, Louis H.
APPLICANT: Peterson, David S.
APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE BINDING PROTEINS
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Patent No. 6632935
Patent No. 6632935
APELICANT: SHIGENOBU, SHUJI
APPLICANT: SHIGENOBU, SHUJI
APPLICANT: HATTORI, MASAHIRA
APPLICANT: SARAKI, YOSHIYUKI
ITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
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MEDIUM TYPE: Floppy disk
COMPUTER: EN PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 10.5EP-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ISFABLICATION NUMBER: 29,655
REGISTRATION NUMBER: 29,655
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Pred. No. 1.3;
0; Mismatches
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                                                                                                                                                                                                                                                                     0; Gaps
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APPLICANT: SHIGENOBU, SHUJI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: WATANABE, HIDEMI
APPLICANT: BAKAKI, YOSHIYUKI
TITLE OF INVENITYON: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
FILE REFERENCE: 081356/0159
CURRENT APPLICATION NUMBER: US/09/790,988
CURRENT FILING DATE: 2001-02-23
PRIOR FILING DATE: 2000-04-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PACENTIN VEY: 2:1
SEQ ID NO 2
LENGTH: 7786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 23.1%; Score 37.4; DB 4; Length 7786; Best Local Similarity 57.1%; Pred. No. 1.9; Matches 68; Conservative 0; Mismatches 51; Indels 0
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; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
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US-09-790-988-2
'Sequence 2, Application US/09790988
; Patent No. 6632935
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; ORGANISM: Buchnera sp.
US-09-790-988-2
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AQ991774 Rfc02039F
AQ991791 Rfc02368F
AQ990809 Rfc01638
AQ990869 Rfc01706
                                                                            September 9, 2004, 17:30:16; Search time 1308.61 Seconds (without alignments) 3696.811 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                     27513289 seqs, 14931090276 residues
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Maximum Match 100%
Listing first 45 summaries
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AQ991791
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162
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A0991774 770 bp DNA linear GSS 14-AUG-2000		sequence.	AQ991774.1 GI:9650368	GSS.	Photorhabdus luminescens	Photorhabdus luminescens	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;	Enterobacteriaceae; Photorhabdus.
RESULT 1 AQ991774/C LOCUS	DEFINITION	NOTRABLOM	VERSION	KEYWORDS	SOURCE	ORGANISM		

REFERENCE 1 (bases 1 to 770)
AUTHORS ffrench-Constant, R. H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P. J., Bowen, D. and Blattner, F. R.
TITLE A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
JOHNAL Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
MEDLINE 20378633
PUBMED 10919786
COMMENT Contact: ffrench-Constant RH
COMMENT Department of Biology and Biochemistry
University of Bath
South Building, Bath BAZ 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826729

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Acids Res.
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AQ990809/c
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 82673
Email: bssrfc@bath.ac.uk
This is one of a selected subset of flipped clones from the M13
library. For annotation of identified clones (BLASIX, BLASIX and mapping to E. coli K12 genome) please see ffrench-Constant et al.
2000, Nucleic Acids Res.
Seq primer: M13 Reverse
Class: Shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS 14-AUG-2000
                                                                                                                                                                                                                                                                                                                         /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         french-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium bytornabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Photorhabdus luminescens
Bacteria; Protecbacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
           This is one of a selected subset of flipped clones from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. Seg primer: M13 Reverse Class: shotgun.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REC02368F Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02368F, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                       /db_xrefe"taxon:29488"
/clone="PLG02039F"
/dv_stage="primary phase variant"
/clone lib="Photorhabdus luminescens strain W14 M13
                                                                                                                                                                                                                                                                                                                                                                                                  Length 770;
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                                                                                                                                                                   'organism="Photorhabdus luminescens"
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; Pred. No. 7.3e-22;
0; Mismatches 0;
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                                                                                                                                                                                     /mol_type="genomic DNA"
/strain="W14"
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                                                                                                                               Location/Qualifiers
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Smail: bssrfc@bath.ac.uk
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AQ991791.1 GI:9650385
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Best Local Similarity 100.0%;

Matches 162; Conservative 0
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A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Rfc01638 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01638, genomic survey
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ffrench-Constant,R.H., Waterfield,N., Burland,V., Perna,N.T.,
                                                                                                                                        /dev_stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
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/clone="pLG01638"
/dev_xelga="primary_phase_variant"
/clone_lib="Photorhabdus_luminescens_strain_W14_M13_
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organism="Photorhabdus luminescens"
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100.0%; Pred. No. 7.2e-22;
iive 0; Mismatches 0;
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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                  /mol_type="genomic DNA"
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/strain="W14"
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/clone="PLG02368F"
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Enterobacteriaceae, Photorhabdus.
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Photorhabdus luminescens genomic clone PLG01706, genomic survey
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                                                                                       28; Length 712;
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Pred. No. 1.5e-21;
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Department of Biology and Biochemistry
University of Bath
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/strain="W14"
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/clone="PLG01706"
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Fax: (44) 1225 826779
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Hayashizaki,Y. Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)

Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Contributed to
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AGENCOURT 15225345 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001697
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1 (bases 1 to 827)
NIH-MGC http://mgc.ncl.nih.gov/.
NIH-MGC http://mgc.ncl.nih.gov/.
Outional Institutes of Health, Mammalian Gene Collection (MGC) Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="18 days embryo"
/clone lib="RIKEN full-length enriched, 18 days embryo
whole body"
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
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Bldg. 31 RmL0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
CDNA Library Preparation: Open Biosystems
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Pred. No. 3.4e-20;
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/clone="L430040C03"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J"
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96.9%;
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Best Local Similarity
Matches 157; Conserva
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/tissue_type="whole body"
/lab_host="NBLDB"
/lab_host="NBLDB"
/clone_lib="WH ZGC_10"
/note="Vector: pExpress; Site_1: Not!; Site_2: EcoRV;
/note="Vector: pExpress; Site_1: Not!; Site_2: EcoRV;
/note="Vector: person strain. is terrand cDNA was primed a Not 1 - oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A normalized version of this library is also available (NHH ZGC 7). Library was constructed by Open Blosystems (Huntsville, AL)."
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1 (bases 1 to 787)

1 With-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm.DAD7 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Preparation: Open Blosystems
CDNA Library Preparation: Open Blosystems
CDNA Library Arrayed by: The I M.A.G.E. Consortium (LLNL.)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAMM4695 row: g column: 08
High quality sequence start: 26
High quality sequence stop: 468.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                               /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:7955"
/clone="IMAGE:7001697"
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Danio rerio
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Best Local Similarity 97.5%;
Matches 153; Conservative
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/mol_type="genomic DNA"
organism="Danio rerio"
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Matches 152; Conserv
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                                                                                                                                                                                                                  /dlone_lib="NHF_ZGG_10"
/clone_lib="NHF_ZGG_10"
/note="Vector: pExpress1; Site 1: NotI; Site 2: ECCRV;
Note was collected from a whole adult_individual
from the Tuebingen strain. Ist strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and ECCRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NNH ZGG_7). Library was constructed by Open Biosystems
(Huntsville, AL).
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AGNORT 15225501 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001611
CP347718
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1 (bases 1 to 755)

WH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Daniela (1939)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Preparation: Open Biosystems
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLAM14655 row: c column: 18
High quality sequence stop: 184.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                92.3%; Score 149.6; DB 1497.4%; Pred. No. 1.7e-19; iive 0; Mismatches 4;
  http://image.llnl.gov
Plate: LLAM14695 row: i column: 02
                                                                                                                                                            /clone="IMAGE:7001739"
/tissue_type="whole body"
/lab_host="DH108"
                                                                                                    'organism="Danio rerio"
                                         698.
                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:7955"
                                       High quality sequence stop: (
Location/Qualifiers
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Danio rerio
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Best Local Similarity 97.45
Matches 152; Conservative
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A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Enterobacteriaceae, Photorhabdus.
1 (bases 1 to 756)
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Pred. No. 2.2e-19;
0; Mismatches 5;
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Department of Balology and Blochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 8266779
Email: bssrfc@bath.ac.uk
                                                                                                     /clone="IMAGE:7001611"
/tissue_type="whole body"
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/mol_type="mRNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Photorhabdus luminescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.0%;
nilarity 96.8%;
Conservative 0,
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Library was size-selected for >1 kb fragments. A

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CB403882 583 bp mRNA linear EST 15-MAY-2003
OSTR013H1_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tal: 617 632 5139
Fax: 617 632 5739
Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db xref="taxon:6239"
/sex="Hermaphrodite and male"
/rissue_type="whole animal"
/drow_ctage="mixed stage"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                  66 CAGTATTATGTAGTCTGTTTTTTATGCAAATCTAATTTAATATATTGATATTTATATAT 125
                                                                                                                                                                                                                                                                                                                                                                                                    normalized version of this library is also available (NIH ZGC 7). Library was constructed by Open Biosystems (HunEsville, AL)."
                                                                                                                                                                                                                                                          6 TACAGGICACIAAIACCAICIAAGIAGIIGAIICAIAGIGACIGCAIAIGIIGIGIIIIIA
                                                                                                                                                                                                                                                                                                          39 TACAGGICACIAAIACCAICIAAGIACIIGGIICAIAGGGACIGCCIAIGIIGIGIIIIIA
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                                                                                                                                               85.1%; Score 137.8; DB 14; Length 777; 92.4%; Pred. No. 3.1e-17;
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Rhabditoidea, Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                     12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126 TITIACGTITCTCGTTCAGCTITTTTATACTAACTTG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 rriraccarrerderreaacririrgaacaaacric 195
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                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Marc Vidal Laboratory
Dana Farber Cancer Institute
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/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CB403882.1 GI:30745609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Caenorhabditis elegans
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                                                                                                                                                                                                     Matches 145; Conservative
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                                                                                                                                                                           Best Local Similarity
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CB403882/c
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/note="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV;
Nute="Vector: pExpress1; Site_1: NotI; Site_2: EcoRV;
Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. 1st strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CF347686 777 bp mRNA linear EST 18-AUG-2003
AGENCOURT_15225248 NIH_ZGC_10 Danio rerio cDNA clone IMAGE:7001643
                                                                                                                                       /note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NITH-WGC http://wgc.nci.nih.gov/.

NITH-WGC http://wgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Institute / NIH

Bldg: 31 Rml0A07 Bethead, MD 20892

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard

CDNA Library Preparation: Open Biosystems

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Http://imaga-llnl.gov

Righ quality sequence start: 373

High quality sequence start: 373

High quality sequence story 674.
                                                                                                                                                                                                                                                                                                                                                                                                             509 TITIGITANAGGICACCIAATACCATITAAGIAGITGATTCATAGIGACNGCATATGNIGT 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  449 GITTTACANNANTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTT 390
                                                                                                                                                                                                                                                                                                                                                                  29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 777)
                                                                                                                                                                                                                                                                                                                                                          1 TCTGTTACAGGTCA-CTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGT
/db_xref="taxon:29488"
/clone="PLG00380F"
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/clone_lib="Photorhabdus luminescens strain W14 M13
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                                                                                                                                                                                                                                                     DB 28; Length 756;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 ATATCATTTAGGTTTCTCGTTCAGCTTTTTANACTAACTTG 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120 ATATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAACTTG 162
                                                                                                                                                                                                                                                  Score 140.8; DB 28;
Pred. No. 8.3e-18;
0; Mismatches 9;
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/tissue_type="whole body"
/lab_host="DH10B"
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                  tch 86.9%; al Similarity 93.9%; 153; Conservative
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CF347686
                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 153; Conserv
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CF347686
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TITLE
JOURNAL
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Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Eldson, J.R., Harley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Tolias, P.P., Ptacek, J., Snyder, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., C., elegans Orreame, L., Hill, D.E. and Vidal, M.
                                                                                                                                                                                                                                            EST 15-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="Hermaphodite and male"
/tissue_type="whole animal"
/tissue_type="whole animal"
/dev_tagge="mixed stage"
/clone_lib="AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
Sequence tag of Gateway entry clones. The primers used Nere
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
                                  TTTTACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 120
                                                                                                                                                                                                                                     CB403984 393 bp mRNA linear EST 15-MAY-200
STR01557_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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Pred. No. 1.3e-15; Tindels
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Contact: Vidal M
Marcy Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
TH: 617 632 5180
Fax: 617 632 5739
                                                                                                                      226 TCATTINACGITTCINGTTCAGNITTTTTATACTAAGTTG 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
                                                                                                123 TCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAGCTTG
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                                                                                                                                                                                                                                                                                                           CB403984.1 GI:30745711
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95.0%;
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Best Local Similarity
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CB403984/c
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I (bases I to 395)

I (fases I to 395)

I french-Constant, R. H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 82661
Fax: (44) 1225 826779
Fmail: bssric@bath.ac.uk
This is one of 2,122 random reads from the MI3 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
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                                                                                                                                                                                                         81 TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA 22
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Photorhabdus luminescens genomic clone PLG02205, genomic survey
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/clone lib="Photorhabdus luminescens strain W14 M13
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               DB 14; Length 583;
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0; Mismatches 13
          Score 134.6; DB 1-
Pred. No. 1.4e-16;
0; Mismatches 4;
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/strain="W14"
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/clone="PLG02205"
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AQ991303.1 GI:9649897
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97.2%;
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AQ991303/c
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I (bases 1 to 769)

Ifranch-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, R.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E. coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic Acids Res.
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Rfc01245 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01245, genomic survey
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| mol_type="genomic DNA" |
| strain="denomic DNA" |
| strain="denomic DNA" |
| db_xref="taxon:29488" |
| clone="prG01245" |
| clone="prG01245" |
| clone="primary phase variant" |
| clone="primary phase variant" |
| clone="lb="Photorhabdus luminescens strain W14 M13 |
| library" |
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Class: shotgun.
Location/Qualifiers
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Photorhabdus luminescens
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AQ990470.1 GI:9649064
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GSS 14-AUG-2000

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french-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T., Daborn, P.J., Bowen, D. and Blattner, F.R. Agenomic sample sequence of the entomopathogenic bacterium Photorhabdus luminescens W14: potential implications for virulence Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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Enterobacteriaceae, Photorhabdus.
Rfc01715 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01715, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
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/organism="Photorhabdus luminescens"
/mol trge="genomic DNA"
/strain="W14"
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larity 95.9%; Pred. No. 5.1e-15;
Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AX, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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Job time : 1309.61 secs
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113, App
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                                                                                                                        September 9, 2004, 19:34:38; Search time 204.654 Seconds (without alignments) 3982.858 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                    1 tctgttacaggtcactaata......agcttttttatactaacttg 162
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1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/USO6_NEW PUB.seq:*
4: /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
7: /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/USO8_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/USO9_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/USO0_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
18: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/USO0_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-403-232-175
US-10-403-232-170
US-10-603-232-173
US-10-627-114
US-10-627-711-8
US-09-244-805-57
US-09-244-805-57
US-09-245-277-57
US-10-161-403-113
US-10-161-403-113
US-10-055-001A-25
US-10-055-001A-25
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Maximum Match 100%
Listing first 45 su
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Maximum DB seq length: 200000000
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Perfect
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126 TAICATTITACGTTTCTCGTTCAGCTTTTTTATACTAACTTG 167
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US-10-403-232-173
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Best Local Similarity
                                                                                           US-10-403-232-173
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Publication No. US20040115812A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FANA Shuwei
TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND FILE REPERENCE: 512362 CORRENT APPLICATION NUMBER: US/10/627,711
CURRENT APPLICATION NUMBER: 60/398,589
PRIOR APPLICATION NUMBER: 60/398,589
PRIOR APPLICATION NUMBER: 60/398,589
PRIOR APPLICATION NUMBER: 60/398,589
SRIOR APPLICATION NUMBER: 60/398,589
REOF REAL STATES AND NOS: 24
SOFTWARE: Patentin version 3.2
SEQ ID NO 10
LENGTH: 168
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            Sequence 175, Application US/10403232
Publication No. US20030226164A1
GENERAL INFORMATION:
APPLICANT: Suttie, Janet Louise
APPLICANT: Chilton, Mary-Dell
APPLICANT: Que, Qiudeng
APPLICANT: Que, Qiudeng
APPLICANT: Que, Nary-Dell
APPLICANT: Que, Nary-Dell
APPLICANT: Que, Qiudeng
TITLE OF INVENTION: Lambda Integrase Mediated Recombination In Plants
FILE REFERENCE: 70005USPS
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; Pred. No. 1.4e-25;
0; Mismatches 0;
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100.0%; Score 162; DB 17;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 162; Conservative 0; Mismatches 0;
                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/403,232
CURRENT FILING DATE: 2003-03-28
NUMBER OF SEQ ID NOS: 185
SSQTWARE: PatentIn version 3.2
LENGTH: 166
                                                                                                                                                                                                                                                                                                      TYPE: DNA
, ORGANISM: Bacteriophage lambda
US-10-403-232-175
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Best Local Similarity 100.0%;
Matches 162; Conservative 0
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US-10-627-711-10
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US-10-310-695-14

Sequence 14, Application US/10310695

Publication No. US20040110293A1

GENERAL INFORMATION:

APPLICANT: BROGE, PETER

TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS

FILE REFERENCE: DEBE:019US
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Squence 173, Application US/10403232

Publication No. US20030226164A1

GENERAL INFORMATION:

APPLICANT: Suttie, Janet Louise

APPLICANT: Chilton, Mary-Dell

APPLICANT: Que, Qiudeng

APPLICANT: Que, Qiudeng

TITLE OF INVENTION: Lambond, Anic

TITLE OF INVENTION: Lambond, Anic

CURRENT APPLICANTION NUMBER: US/10/403,232

CURRENT FILING DAIE: 2003-03-28

NUMBER OF SEQ ID NOS: 185

SOFTWARE: Patentin version 3.2

LENGTH: 243
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; NAME/KEY: misc_feature
; LOCATION: (1)...(1763)
; OTHER INFORMATION: y = C or T
; OTHER INFORMATION: n = A,T,C or G
US-09-244-805-57
                                                                  99.0%;
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                                                                  Query Match
Best Local Similarity 99.4
Matches 161; Conservative
OTHER INFORMATION: attp
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ORGANISM: Eukaryote
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  ; US-10-161-403-72
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                                                                                                                                                       Sequence 8, Application US/10627711
Publication No. US20040115812A1
GENERAL INFORMATION:
APPLICANT: YANG, SHUWE!
TITLE OF INVENTION: METHODS AND NUCLEIC ACID VECTORS FOR RAPID EXPRESSION AND TITLE OF INVENTION: SCREENING OF CDNA CLONES
TITLE OF INVENTION: SCREENING OF CDNA CLONES
TITLE OF INVENTION: SCREENING OF CDNA CLONES
TITLE OF INVENTION SCREENING OF CDNA CLONES
TITLE OF INVENTION NUMBER: US/10/627,711
CURRENT APPLICATION NUMBER: US/10/627,711
FRICR APPLICATION NUMBER: 2003-07-26
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 248
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                                  121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAAGTTG 162
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  121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTTATACTAACTTG 162
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APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Elena
APPLICANT: Fleming, Elena
APPLICANT: Shellard, Joan
ITLE OF INVENTION: CHROMSOME-BASED PLATFORMS
FILE PEFERBNCE: 24601-420
CURRENT APPLICATION NUMBER: 00/294,758
PRIOR PILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FLANG DATE: 2002-03-21
SEQ ID NO 72
LENGTH: 282
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Publication No. US20030119104A1
GENERAL INFORMATION:
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ORGANISM: Artificial Sequence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial
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                                                                                                                RESULT 6
US-10-627-711-8
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Publication No. US20030203840A1

GENERAL INFORMATION:

APPLICANT: Worley, Paul F.

APPLICANT: Goetz, Bernard

APPLICANT: Heinimisch, Holger

APPLICANT: Holmisch, Holger

APPLICANT: Scheek, Sigrid

APPLICANT: Scheek, Sigrid

APPLICANT: Nikolich, Karoly

APPLICANT: Nikolich, Karoly

APPLICANT: Nikolich, Kapene

TITLE OF INVENTION: IMMEDIATE EALY GENES AND METHODS OF USE

TITLE OF INVENTION: THEREFOR

FILE OF INVENTION: THEREFOR

FILE REFERENCE: 10496/00401

CURRENT APPLICATION NUMBER: 06/074,518

EARLIER APPLICATION NUMBER: 60/074,518

EARLIER PILING DATE: 1998-02-05

NUMBER OF SEQ ID NOS: 62

SOFTWARE FRIENC DATE: 1998-02-06

SOFTWARE FRIENC DATE: 1998-02-06

SOFTWARE FRIENC DATE: 1998-02-06

SOFTWARE FRIENC DATE: 1998-02-06

SOFTWARE FRIENC DATE: 1998-02-06

SOFTWARE FRIENC DATE: 1998-02-06
Length 282;
                                                                       1; Indels
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Score 160.4; DB 15;
Pred. No. 3.5e-25;
0; Mismatches 1;
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Sequence 113, Application US/10161403 Publication No. US20030119104A1 GENERAL INFORMATION:
                                                        NAME/KEY: misc feature

LOCATION: (1)...(1763)

OTHER INFORMATION: y = C or T

COTHER INFORMATION: n = A,T,C or G
US-10-792-481-57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Artificial Sequence
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Best Local Similarity
                 ORGANISM: Eukaryote
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Sequence 57, Application US/09245277

Publication No. US2003211984A1

Generation No. US20032211984A1

GENERAL INFORMATION:

APPLICANT: Worldy, Paul F.

APPLICANT: Landhan, Anthony

TITLE OF INVENTION: THEREFOR

FILE REFERENCE: JUJ130-3

CURRENT APPLICATION NUMBER: US/09/245,277

CURRENT APPLICATION NUMBER: 06/074,518

PRIOR PLING DATE: 1999-02-05

PRIOR PLING DATE: 1998-02-12

PRIOR PLING DATE: 1998-02-12

PRIOR PLING DATE: 1998-02-15

PRIOR FILING DATE: 1998-02-16

NUMBER OF SEQ 1D NOS: 63

SOFTWARE: FastSEQ for Windows Version 4.0

SEMENT 1902
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Pred. No. 5.9e-25;
0; Mismatches 1; Indels 0;
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| APPLICANT: Worley, Paul F. |
| APPLICANT: Worley, Paul F. |
| APPLICANT: Geetz, Bernard |
| APPLICANT: Geetz, Bernard |
| APPLICANT: Geetz, Bernard |
| APPLICANT: Heimisch, Holger |
| APPLICANT: Scheek, Sigrid |
| APPLICANT: Scheek, Sigrid |
| APPLICANT: Nikolich, Karoly |
| APPLICANT: Nikolich, Karoly |
| APPLICANT: NIWENICON: IMMEDIATE EARLY GENES AND METHODS OF USE |
| TITLE OF INVENTION: THEREFOR |
| TITLE OF INVENTION: THEREFOR |
| TITLE OF INVENTION: THEREFOR |
| FILE REFERENCE: 10496/004001 |
| CURRENT APPLICATION NUMBER: US/09/244,805 |
| PRIOR FILING DATE: 1999-02-05 |
| PRIOR FILING DATE: 1998-02-12 |
| PRIOR FILING DATE: 1998-02-12 |
| PRIOR FILING DATE: 1998-02-12 |
| PRIOR FILING DATE: 1998-02-06 |
| NUMBER OF SEQ ID NOS: 62 |
| SOFTWARRE: FastSEQ for Windows Version 4.0 |
| SEQ ID NO 57 |
| LENGTH: 1763
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OTHER INFORMATION: \gamma = C or T
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 99.4%;
Matches 161; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Eukaryote
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US-10-792-481-57/c
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       Length 1763;
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Query Match
99.0%; Score 160.4; DB 17; Length
Best Local Similarity 99.4%; Pred. No. 5.9e-25;
Matches 161; Conservative 0; Mismatches 1; Indels
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APPLICANT: Perfact, Carally
APPLICANT: Greene, Amy
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
APPLICANT: Leung, Josephine
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-403
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER: OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 24, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Weeley, Susan V.
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Using recombinational cloning
TITLE OF INVENTION: Using recombinational cloning
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT PILING DATE: 2002-06-11
SOFTWARE: PatentIn version 3.1
SEQ ID NO 24
                                                                                                                                                                                                                                                                                                APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: using recombinational cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13128 TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATGTATTTA 13069
16578 TTTTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGTATTTA 16637
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Pred. No. 5.8e-23;
0; Mismatches 6; Indels
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Pred. No. 5.8e-23;
0; Mismatches 6; ]
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                                                                                                                                                                                                                                                                                                                                                                                                                        FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                               US-10-055-001A-25/c
; Sequence 25, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
                                               121 TATCATITIACGITICICGITCAGC
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Best Local Similarity 96.3%;
Matches 156; Conservative
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Best Local Similarity 96.3%;
Matches 156; Conservative
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LENGTH: 17458
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US-10-055-001A-24
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GUNERAL INFORMATION:

APPLICANT: Waterhouse, Peter
APPLICANT: Hellivell.(christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: Waing recombinational cloning
FILE REFERENCE: HELLGA
CURRENT FILING NAMBER: US/10/055,001A
CURRENT FILING NAMBER: 202-06-11
NUMBER OF SEQ ID NOS: 26
SSOFTWARE: PatentIn version 3.1
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                                                       Sequence 2, Application US/10310695
Publication No. US20040110293A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: BRENKEL, BARBARA
TITLE OF INVENTION: SEQUENCE SPECIFIC DNA RECOMBINATION IN EUKARYOTIC CELLS
FILE REPERENT APPLICATION NUMBER: US/10/310,695
CURRENT APPLICATION NUMBER: US/10/310,695
CURRENT FILING DATE: 2002-12-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 243
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US-10-055-001A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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Matches 158; Conservative
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LENGTH: 17458
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Maximum Match 100%
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RESULT 1 AX092115 LOCUS DEFINITION ACCESSION VERSION KEYWORDS	AX092115 162 bp DNA linear PAT 21-MAR-2001 Sequence 4 from Patent WO0116345. AX092115. AX092115.1 GI:13444358
SOURCE	Escherichia coli Escherichia coli
	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae: Escherichia
REFERENCE	
AUTHORS	Droege, P.
TITLE	Sequence-specific dna recombination in eukaryotic cells
JOURNAL	Patent: WO_0116345-A 4 08-MAR-2001;

PAT 21-MAR-2001

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ILAMINITATT 361 bp DNA linear PHG 28-APR-1993

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                                                                                                                                 Bacteriophage lambda
Bacteriophage lambda
Viruses; pADNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
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                                                                                                                                                                                                                                                                                         Sequence-specific dna recombination in eukaryotic cells Patent: WO 0116345-A 2 08-MAR-2001; Droege, Peter (DE) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 243;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.0%; Score 160.4; DB 6; Best Local Similarity 99.4%; Pred. No. 1.3e-20; Matches 161; Conservative 0; Mismatches 1;
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Pred. No. 1.2e-20;
0; Mismatches 1.
     DNA
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/mol_type="unassigned DNA"
/db_xref="taxon:10710"
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/mol_type="genomic DNA"
/db_xref="taxon:10710"
AX092113 243 bp
Sequence 2 from Patent WO0116345.
AX092113
                                                                                AX092113.1 GI:13444356
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84242838
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Bacreriophage lambda site specific recombinant DNA (attR).
M12459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Original source text: Bacteriophage lambda DNA.
Circular phage DNA (attP) and linear bacterial DNA (attB) undergo
integrative recombinations to yield attL and attR. AttL and attR
can undergo excisive recombination. Positions 159-165 demark the 7
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Viruses, dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;
Lambda-like viruses.
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                                                                                                                                                                                                                       Length 162;
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Bushman, W., Thompson, J.F., Vargas, L. and Landy, A.

Control of directionality in lambda site specific

Science 230 (4728), 906-911 (1985)
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100.0%; Score 162; DB 7;
Best Local Similarity 100.0%; Pred. No. 7.1e-21;
Matches 162; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 7.2e-21;
ive 0; Mismatches 0;
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/mol_type="genomic DNA"
/db xref="taxon:10710"
                                                                                                           /mol_type="unassigned DNA"
/db_xref="taxon:562"
                                                                                organism="Escherichia"
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Location/Qualifiers
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     Peter (DE)
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Matches 162; Conservative
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        Droege,
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PC C12N15/00,C12N5/00
CC n is either a
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                                                                                                                                          sex="male"
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  Fax:+81-426-76-4517)
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Submitted (23-MAY-1996) Kenichiro Ogura, Tokyo University of
Bubmitted and Life Science, Department of Drug Metabolism and
Molecular Toxicology; 1432-1 Horinouchi, Hachioji, Tokyo 192-0392,
Japan (E-mail:ogurak@ps.toyaku.ac.jp, Tel:+81-426-76-4518,
                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, asterids, lamiids, Solanales, Solanaceae, Nicotiana.
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TITIACAGTATTATGTAGTCTGTTTTTTTTGCCAAAATCTAATTTAATATATTGATATTTT 140
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hydroxysteroid sulfotransferase subunit.
hydroxysteroid sulfotransferase subunit.
Macaca fascicularis
Macaca fascicularis
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
1 (bases 1 to 1668)
Ogura, K., Satsukawa, M., Kato, K., Okuda, H. and Watabe, T.
Molecular cloning of monkey liver hydroxysteroid sulfotransferase
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Macaca fascicularis mRNA for hydroxysteroid sulfotransferase
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.larity 99.4%; Pred. No. 1.1e-20;
Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                   linear
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                                                                                                  98
                                                                                139 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAAGTTG
                                                             121 TATCATTTTACGTTCTCGTTCAGCTTTTTTATACTAACTTG
                                                                                                                                                                                                   DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Nicotiana tabacum"
/mol_type="unassigned DNA"
/db_xref="taxon:4097"
                                                                                                                                                                                                                                                                                                                                                                                                                                      Targeted gene removal
Patent: WO 0121780-A 1 29-MAR-2001;
THE UNIVERSITY OF LEEDS (GB)
                                                                                                                                                                                                                                                                                                  Nicotiana tabacum (common tobacco)
                                                                                                                                                                                           610 bp
Sequence 1 from Patent WO0121780.
AX101000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                     Meyer, P.L. and Zubko, E.L.
                                                                                                                                                                                                                                                         AX101000.1 GI:13619857
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2 (bases 1 to 1668)
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Matches 161; Conserv
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                        199
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TITLE
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TITLE
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VERSION
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MACHSS/c
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OLFPKSFFSSKAKVIYLMRNPRDVFVSGYFFWNSVKFVKKFKSWQQYFEWFCGGNVIY
GSWPDHIHGMMPMREKKNFLLLSYBELKQDTRRTVEKTCGFLGKTLEPBELNLILKNS
SPGSMKENKMSNFSLLSVDFVBEKAQLLRKGISGDWKNHLIVAQAEAFDKLFQBKMTD
LPRELFPWE"
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                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MSDDFLWFEGIAFPNMGFRSFTLRKVRDEFVIKDEDVIILTYPK
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                                                                                                                                                                                                                                                                                                                                                                                                                                        SGINWLIEILCLIHSNGDPKWIQSVPIWERSPWVETEMGYKLLSEEEGPRLFSSHLPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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CI2N15/09,A61K31/711,A61K48/00,A61P25/00,A61P25/28,C07H21/04, PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              331 TITTACAGTATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
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PN 07 2002512772-A/49
PD 08-MAZ-2002
PF 05-FEB-1999 UP 2000530634
PR 09-FEB-1999 US 60/074135,12-FEB-1999 US 60/074518
PR 09-FEB-1998 US 60/074135,12-FEB-1998 US 60/074518
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                         /codon_start=1
/product="hydroxysteroid sulfotransferase subunit"
/protein id="BAAl2823.1"
/db_xref="GI:1345406"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Worley, P.F., Lanahan, A., Goetz, B., Hiemisch, H., Kuner, R., Scheek, S., Nikolich, K. and Zhukovski, B.
Immediate early gene and method for using the same parent: JP 2002512772-A 49 08-MAY-2002;
THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE, BASF LYNX BIOSCIENCE AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ·;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 160.4; DB 9; Length 1668; Pred. No. 8.5e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ווהearly gene and method for using the same.
BD225932
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            271 TATCATTTTACGTTTCTCGCTTCAGCTTTTTTATACTAAGTTG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 TATCATTTTACGTTTCTCGTTCAGCTTTTTTATACTAACTTG 162
                                                              /organism="Macaca fascicularis"
/mol_type="mRNA"
/db_xref="taxon:9541"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                   tissue type="liver"
/clone lib="lambda gtll"
611. .1468
Location/Qualifiers
1. .1668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rattus norvegicus (Norway
Rattus norvegicus
                                                                                                                                                 clone="monHST-1"
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or

us-10-082-772b-4.rge

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/trānslation="MYLFIYIFFFFFFFFFVIVQKDIEQLDIKCAHEQMNIQKQYDE
KKKPLFEKREDEIQKIPGFRAMTLKKHPALSDIVPEDIDILMHLWKLDIKDNMDNNGS
YKITFIFGEKAKEFMEPLIVKHVTFDNNQEKVVECTRIKWKEGKNPIAAVTHNRSDL
DNBIPKWSIFEWFTTPDELQDKPDVGBLIRREIWHNPLSYYLGLEEFDBFDDDFDEFFD
DDDDDDDDDDDDDDDDKDDDLGDDDGNNDDND"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF178449 3485 bp DNA linear SYN 20-JUL-2000 Integration vector pCD11PKS chloramphenicol transacetylase (cat) and beta-galactosidase alpha peptide (lacZa) genes, complete cds. AF178449
                                                                                                                                                                                                                                                                                                                                                                                                                                        'translation="MVLVTCNRALAQGDFCLLALIFCHQTCRTPEKHKASQSSAKLVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="PQYQFVGAKLFRWWCWRRRGWRRRWWLVIKLMLIETSFALDCEA
LCFSGVRQV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2488 ITITACAGTATTATGTAGTGTTTTTTTTTTTTTTTTATGCAAARTCTAATTTAATATTTTTTTTA 2429
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Integration vector pCD11PKS
artificial sequences; vectors.

1 (Dases 1 to 3482)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and lac2 gene fusions into the Escherichia coli chromosome Plasmid 43 (1), 12-23 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITIACAGIATTATGTAGTCTGTTTTTTATGCAAAATCTAATTTAATATTGATATTTA
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                                                                                                                                                                                                                       complement(2141. .2650)
/note="putative VECTOR sequence Bacteriophage lambda
(J02459); putative"
2525. .2758
/gene="histidine rich protein C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                           product="histidine rich protein C"
protein id="AAA29621.1"
db xref="G1:160343"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             INISLITSHHRLRHPRRRQHHHRNNFAPTNWYWG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="histidine rich protein
/protein_id="AAA29622.1"
/db_xref="G1:160344"
                                                                 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (2596. .2758)

Gapte="Mistidine rich protein D"
complement (5596. .>2758)
/gene="histidine rich protein D"
                            'gene="histidine rich protein E"
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Pred. No. 7.6e-21;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                       2525. .>2758
/gene="histidine rich protein
                                                /codon_start=1
/product="histidine rich
/protein_id="AAA29620.1"
/db_xref="GI:160342"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon_start=2
                                                                                                                                                                                                                                                                                                                                                             codon_start=1
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Best Local Similarity 99.4
Matches 161; Conservative
                                                                                                                                                                                                                           misc feature
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AUTHORS
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TITLE
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AF178449
LOCUS
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KEYWORDS
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histidine-rich protein.
Plasmodium falciparum (malaxia parasite P. falciparum)
Plasmodium falciparum
Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 2758)
Lenstra,R., d'Auriol,L., Andrieu,B., Le Bras,J. and Galibert,F.
Cloning and sequencing of Plasmodium falciparum DNA fragments
containing repetitive regions potentially coding for histidine-rich
proteins: identification of two overlapping reading frames
Blochem. Blophys. Res. Commun. 146 (1), 368-377 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="histidine rich protein B"
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                                                                                                                                                                                                                                           ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="DPYKERIKSDIRQINESQYLKSLAYKYISGEDYTQYLLLNEVLK
DDQDYCTCTRRTIYEESMDNTVEFAKKAYYELSA"
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                                                                                                                                                                                                                                                                                                                                                                                                  312
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                                                                                                                                                                                                                                                                                                                                                                                          371 TITIACAGIAITAIGIAGICIGITITITAIGCAAAAICIAATITIAATAITAATITIA
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                                                                                                                                                                                                                                             Gaps
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Location/Qualifiers
1. .2758
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0
                                                                                                                                                                                                     Length 1763;
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complement (828 . .1589)
/gene="histidine rich protein E"
complement (828 . .1589)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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                                                                                                                                                                                                     DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Plasmodium falciparum"
/mol_type="genomic DAA"
/db_xref="taxon:5833"
1. .234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   гланкРС
P.falciparum histidine-rich protein genes.
M17028
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| gene="histidine rich protein B"
Location/Qualifiers
Location/Qualifiers
Location/Qualifiers
1. .1763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="histidine rich protein A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene="histidine rich protein B"
                                                                                                                                                                                                                       8.4e-21;
                                                                                               /organism="Rattus norvegicus"
/mol type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <1. .234
/gene="histidine rich protein</pre>
                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                   99.0%; Score 160.4; 99.4%; Pred. No. 8.4e
                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MEKKITGYTTVDISQWHRKEHFEAPQSVAQCTYNQTVQLDITAF
LITYVKKNRHKEYPAFHILARLMNAHPERMANGGELVINDSVHPCYTVFHEQTETF
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ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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ARTDRPSQQLRSLNGEWLTRPVAAH"
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(18-AUG-1999) Microbiology, Iowa State University, 207 Building, Ames, IA 50011, USA Location/Qualifiers
                                                                                                                                                                                                                     /note="attP; attachment site from bacteriophage lambda"
complement(1327. .1986)
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Integration vector points.
artificial sequences; vectors.
1 (bases 1 to 3485)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    673 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              producE="beta-galactosidase alpha peptide"
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db_xref="GI:9294786"
                                                                                                                                                                                                                                                                                                                       /codon_start=1
/trans1_table=11
/producE="chloramphenicol transacetylase"
/protein_id="AARB6671.1"
/db_xref="GI:9294787"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTTTATACTAACTIG 162
                                                                            /organism="Integration vector pCD11PKS"
mol_type="genomic DNA"
db_xref="taxon:106602"
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/note="multiple cloning site"
                                                                                                                                  /lab host="Escherichia coli"
1. 385
/note="R6Kgamma"
                                                                                                                                                                                                                                                                                  complement (1327. .1986)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="lacza"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="lacZa"
                                                                                                                                                                                                                                                                                                    gene="cat'
                                                                                                                                                                                                                                                                 /gene="cat
                                                                                                                                                                                                     668. .915
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/protein_id="AAF86673.1"
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ANMDNFFAPVFTMGRKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNBLQQXCDBWQGG
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IPSTSRGGPVPNSPYSESYYARSLAVULQRRDWENPGVTQLNRLAAHPPFASWRNSEE
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lacZ gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
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Pred. No. 7.2e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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/lab host="Escherichia coli"
1. .385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .1986)
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complement (2754.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (1327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           table=11
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/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="R6Kgamma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="cat"
/codon_start=1
/trans1_table=1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="lacZa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cloning vector pLDR9, o
AF271663
AF271663.1 GI:9022390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 161; Conservative
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pExCell cloning vector, complete sequence
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                   U13848
U13848.1
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 DEFINITION
                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                      TITLE
JOURNAL
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                   ACCESSION
                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
                                     VERSION
KEYWORDS
                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                          TITLE
                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IEIDINSGKILESFRPBERFPPWSTFKVLLCGAVLSKVDAGGEOLGRRIHYSQNDLVE
SYDTEKHLTDOMTVRELCAAITWONTAANLLITTIGGREIHENGDHYTRL
DRWEPELNEAI BYDDREDTYMPYARINKLITGELLTASROOL IDWMEAVVAGPL
IRSALPAGWFIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATWDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AaF82364.1"
/db_xref="G1:9022393"
/translation="MIPRDPRSPAPDLSAINQPAGRAERRSGPATLSASIQSINCCRE
ARVSSSPVNGLRNVYAIATGIVVSRSSFGMASFSSGSQRSRRVT"
                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MSHIQRETSCSRPRLNSNMDADLYGYKWARDNVGQSGATIYRLY
GKPDAPELFLKHGKGSVANDVTDEMVRLNWLTEFMPLPTIKHFIRTPDDAWLLTTAIP
                                                                                                                                                                                                                                                                                                                                                                                                                                     GKTAFQVLEEYPDSGENIVDALAVFLRRLHSIFYCNCPFNSDRVFRLAQAQSRMNGL
VDASDFDDERNGWPVEQVWKEMHKLLPFSPDSVVTHGDFSLDNLIFDEGKLIGCIDVG
RVGIADRYQDLAILWNCLGEFSPSLQKRLFQKYGIDNPDMNKLQFHLMLDEFF"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2617 ICTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG 2676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           intracadiatraticadicidiririrangcaaarichariraaridariingaratria 2736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120
                                                     1 (bases 1 to 4105)
Mencis,A.M., Keagle,P., Andersen,J., Wotanis,J., Newcombe,R. and August,P.R.
Direct Submission
Submitted (24-MAY-2000) Molecular Genomics, Aventis
Pharmaceuticals, 26 Landsdowne Street, Cambridge, MA 02139, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITIBACAGTATTATGTAGTCTGTTTTTTTATGCAAAATCTAATTTAATATTGATATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                         product="aninoglycoside 3' phosphotransferase"
protein id="AAF82363.1"
db_xref="GI:9022392"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4105;
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                                                                                                                                                                                                                                                                    216. .1031
/function="confers kanamycin resistance"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAICATITITACGITICICGITCAGCITITITATACIAACTIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="hypothetical 9.2 kD protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 160.4; DB 12;
Pred. No. 6.9e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                        organism="Cloning vector pLDR9"
mol_type="genomic DNA"
db_xref="taxon:130501"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "EC_number="3.5.2.6"
note="derived from pMMB66EH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
transl_table=11
product="beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein_id="AAF82362.1"
db_xref="GI:9022391"
                 Cloning vector pLDR9 artificial sequences; vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="unknown"
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                                                                                                                                                                                                                                                                                                                           table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon start=1
transl table=
                                                                                                                                                                                                                                                                                                         codon start=1 trans table=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99.0%;
99.4%;
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/note="attP"
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   Cloning vector pldR9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                        ...4105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 161; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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XXU13848/c
LOCUS
                                                                                                                                                                                            source
                   ORGANISM
                                                                           AUTHORS
                                                         REFERENCE
                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                      CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
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DRWEPELNEAIPNDERDTTMPVAMATTLRKLITGELLTLASRQQLIDWMEADKVYKU
LRSALPAGNFIADKSGAGERGSRGIIAALGPDGKFSRIVVIYTTGSQATMDERNRQIA
EIGASLIKHW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IELDLNSGKI LESFRPEERFPMMSTFKVLLCGAVLSRI DAGQEQLGRRIHÝSQNDLVE
YSPVTEKHLTDGMTVRELCSAAI TMSDNTAANLLLTTI GGPKELTAFLHNMGDHVTRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="plasmid origin of replication; base 1653 represents
the first base of the newly synthesized strand"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Multiple Cloning Site (MCS); contains unique sites for Sfil, Xhol, EcoRI, BamHI, NotI, MluI, HindIII" complement (2155. .2174)
/gene="T7 RNA polymerase"
/gene="T7 RNA polymerase"
/gene="T7 RNA polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             translation="MSIQHFRVALIPFFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MTMITPSYLGDTIEYRPRGPNSVSGSDTAAARVSFPIVSRITQF
                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (19-AUG-1994) James A. Malone, International Technical
Services, Molecular Biology Reagents Division, Pharmacia Biotech
Inc., 2202 N. Bartlett Ave., Milwaukee, WI 53202-1009, USA
Location/Qualifiers
                                                                                                                                                                                         pExcell: A multifunctional cloning vector that is released from lambda Excell by in vivo excision Unpublished (1994)
2 (bases 1 to 4190)
                         T7 promoter; SP6 promoter; beta-lactamase, lacZ alpha peptide,
                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/lab_host="Escherichia coli"
34. 894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  repressor protein"
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|trans1_table=11
|producf="lanca alpha peptide"
|protein_id="AAA57084.1"
|db_xref="GI:595703"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2073. .2089
/gene="SP6 RNA polymerase"
2073. .2089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene="SP6 RNA polymerase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    codon_start=1
|transl_table=11
|product="beta-lactamase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein_id="AAA57085.1"
db_xref="G1:595704"
                                                                                                                        artificial sequences; vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="lac operator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="lac promoter"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bound_moiety="lacI
                                                                      unidentified cloning vector unidentified cloning vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /direction=right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34. .894
/gene="bla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2013. .2033
/gene="lac"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="bla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001. .2007
/gene="lac"
                                                                                                                                         1 (bases 1 to 4190)
Malone, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'gene="lac"
GI:595702
                                                                                                                                                                                                                                                                                   Malone, J.A.
Direct Submission
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rep\_origin

circular SYN 13-DEC-1994

DNA

4190 bp

XXU13848

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Integration vector pCD13PKS aminoglycoside adenyltransferase (aadA) and beta-galactosidase alpha peptide (lacZa) genes, complete cds. AF178452.1 GI:9294794
                                                                                                                                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                                 09
/note="bacteriophage fl origin of replication for
production of shale-stranded DNA; base 2933 represents
the first base of the newly synthesized single strand"
/direction=right
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dlatt, R., Drescher, C., Park, S.K. and Phillips, G.J.
Direct Submission
Submitted (18-840-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="attP; attachment site from bacteriophage lambda"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Integration vector pCD13PKS
Integration vector pCD13PKS
artificial sequences; vectors.

1 (bases 1 to 4549)
Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Genetic system for reversible integration of DNA constructs and lacZ gene fusions into the Escherichia coli chromosome Plasmid 43 (1), 12-23 (2000)
                                                                                                                                                                                                                                                                                                                                                 1 TCTGTTACAGGTCACTAATACCATCTAAGTAGTTGATTCATAGTGACTGCATATGTTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                            61 TITITACAGTATTATGTAGTCTGTTTTTATGCAAAATCTAATTTAATATTGATATTTA
                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                       DB 12; Length 4190;
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|trans1_table=11
|product="aminoglycoside adenyltransferase"
|protein_id="AAF86677.1"
|db_xref="GI:9294796"
                                                                                                                                                                                                                                                                                                           Indels
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    4549
    organism="Integration vector pCD13PKS"

                                                                                                                                                                                                                                                                     Score 160.4; DB 12;
Pred. No. 6.9e-21;
0; Mismatches 1;
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                                                                                                                                                  /mote="attP gene from lambda"
3932. 3947
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3847. .4094
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Best Local Similarity 99.4%;
Matches 161; Conservative
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Platt,R., Drescher,C., Park,S.K. and Phillips,G.J.
Direct Submission
Submitted (18-440-1999) Microbiology, Iowa State University, 207
Science I Building, Ames, IA 50011, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 4549)
Platt, R., Drescher, C., Park, S. K. and Phillips, G.J.
Genetic system for reversible integration of DNA constructs and lacz gene fusions into the Escherichia coli chromosome
Plasmid 43 (1), 12-23 (2000)
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complement(1798. .2652)
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1. .385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 160.4; DB 12;
Pred. No. 6.8e-21;
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Integration vector pCD13PSK
artificial sequences; vectors.
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AF178453
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4038. 4145
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99.0%; Score 160.4; DB 12; Length 4549;
Best Local Similarity 99.4%; Pred. No. 6.8e-21;
Matches 161; Conservative 0; Mismatches 1; Indels 0;
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Chitobiase as a reporter enzyme
Patent: WO 0127322-A 13 19-APR-2001,
Elitra Pharmaceutigals, Inc. (US)
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Sequence 13 from Patent
AX113748
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                gene="aadA"
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